

SCORE Search Results Details for Application 10591347 and Search Result 20110118_090620_us-10-591-347-2.rng.

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This page gives you Search Results detail for the Application 10591347 and Search Result 20110118_090620_us-10-591-347-2.rng.

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GenCore version 6.3

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OM nucleic - nucleic search, using sw model

Run on: January 18, 2011, 09:09:15 ; Search time 488 Seconds
(without alignments)
148827.160 Million cell updates/sec

Title: US-10-591-347-2
Perfect score: 3424
Sequence: 1 aggatcagaacaatgcctcc.....taaactagttcatttcaaaa 3424

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18225500 seqs, 10608060480 residues

Total number of hits satisfying chosen parameters: 36451000

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_201023:*
1: geneseqn1:*
2: geneseqn2:*
3: geneseqn3:*
4: geneseqn4:*
5: geneseqn5:*
6: geneseqn6:*
7: geneseqn7:*
8: geneseqn8:*

9: geneseqn9:*

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3424	100.0	3424	1	AAS14365	Aas14365 cDNA enco
2	3424	100.0	3424	1	ABL59523	Ab159523 Human pho
3	3424	100.0	3424	2	ADE85076	Ade85076 Farnesyl
4	3424	100.0	3424	4	ADZ00490	Adz00490 p110-beta
5	3424	100.0	3424	4	AEH10445	Aeh10445 PK3CA cD
6	3424	100.0	3424	4	AED31618	Aed31618 cDNA (SEQ
7	3424	100.0	3424	4	AEG93388	Aeg93388 Human tum
8	3412	99.6	3412	1	AAQ51156	Aaq51156 Human p11
9	3412	99.6	3412	4	AED31617	Aed31617 cDNA (SEQ
10	3412	99.6	3423	3	ADU05935	Adu05935 Novel bro
11	3339.6	97.5	3426	6	ARC02473	Arc02473 DNA fragm
12	3339.6	97.5	3724	4	AEK54940	Aek54940 Human PIK
13	3339.6	97.5	3724	5	AER29796	Aer29796 Breast ca
14	3339.6	97.5	3724	7	ARV60468	Arv60468 Human PIK
15	3339.6	97.5	3724	7	ARW65283	Arw65283 Human PIK
16	3339.6	97.5	3724	7	ATM52123	Atm52123 Human PIK
17	3339.6	97.5	3724	7	ATS16021	Ats16021 Human pho
18	3339.6	97.5	3724	8	AWY98731	Awy98731 Human PIK
19	3339.6	97.5	3724	8	AWY98891	Awy98891 Human PIK
20	3339.6	97.5	3724	8	AWY98894	Awy98894 Human PIK
21	3339.6	97.5	3724	9	AXU25358	Axu25358 Human pho
22	3339.6	97.5	3724	9	AYE41305	Aye41305 Human PIK
23	3281	95.8	4326	8	AWY98838	Awy98838 Human PIK
24	3207	93.7	3207	2	ADH68168	Adh68168 DNA encod
25	3207	93.7	3207	4	AEF64785	Aef64785 Human pho
26	3146.6	91.9	7923	8	AWO77361	Awo77361 Expressio
27	3146.2	91.9	3207	7	ARL60529	Arl60529 Human pho
28	3144.6	91.8	3207	4	AEK13519	Aek13519 Phosphati
29	3143	91.8	3207	4	AEK13514	Aek13514 Phosphati
30	3143	91.8	3207	4	AEK13515	Aek13515 Phosphati
31	3138.6	91.7	3498	1	AAQ57012	Aaq57012 PtdIns 3-
32	3120.4	91.1	3210	4	AEK13511	Aek13511 Phosphati
33	3008.6	87.9	3207	1	AAQ51155	Aaq51155 p110 cDNA
34	2642.2	77.2	3207	8	AWY98836	Awy98836 Human PIK
35	2642.2	77.2	3207	8	AWY98892	Awy98892 Human PIK
36	1687.6	49.3	8421	2	ACN43202	Acn43202 Human dia
37	1515.8	44.3	2397	1	AFS82080	Afs82080 Human tra
38	1183.4	34.6	1792	3	ADR39810	Adr39810 Human kin
39	699	20.4	2872	8	AWY98893	Awy98893 Human PIK
40	564	16.5	741	1	AAA02190	Aaa02190 Human col
41	564	16.5	741	4	AGD33161	Agd33161 Human pol
42	530	15.5	716	4	AEK18520	Aek18520 Human PIK
43	460.8	13.5	3213	1	AAC65690	Aac65690 Human PI3

44	460.8	13.5	3213	1	AAS14366	Aas14366 cDNA enco
45	460.8	13.5	3213	1	ABV78026	Abv78026 Hypoxia-r

ALIGNMENTS

RESULT 1

AAS14365

ID AAS14365 standard; cDNA; 3424 BP.

XX

AC AAS14365;

XX

DT 11-JUN-2007 (revised)

DT 12-MAR-2002 (first entry)

XX

DE cDNA encoding human p110alpha isoform of PI3-kinase.

XX

KW Human; phosphatidylinositol 3-kinase; PI3K; p110alpha isoform; LASP-1;

KW cancer; inflammatory disease; ophthalmic disorder; SH3 domain;

KW autoimmune disease; inflammatory bowel disease; bacterial pneumonia;

KW Type I diabetes mellitus; cytostatic; immunosuppressive; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 13..3219

FT /*tag= a

FT /product= "p110alpha isoform of PI3-kinase"

XX

PN WO200185986-A2.

XX

PD 15-NOV-2001.

XX

PF 10-MAY-2001; 2001WO-US015065.

XX

PR 10-MAY-2000; 2000US-0203346P.

XX

PA (ICOS-) ICOS CORP.

XX

PI Sadhu C;

XX

DR WPI; 2002-075252/10.

DR P-PSDB; AAU09687.

DR PC:NCBI; gi472990.

DR PC_ENCPRO:NCBI; gi472991.

XX

PT Identifying a modulator of p110delta polypeptide binding to SH3 domain-
 PT containing polypeptides e.g. LASP-1, comprising allowing the binding

http://es.ScoreAccessWeb/GetItem.action?AppId=1059134...118_090620_us-10-591-347-2.rmg&ItemType=4&startByte=0 (4 of 96)2/3/2011 1:56:01 PM

Db	241	GCAGAAAGGGAAGAATTTTTTGTATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTTCAA	300
Qy	301	CCATTTTTTAAAGTAATTGAACCAAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Db	301		360
Qy	361	ATTGGTTTTGCTATCGGCATGCCAGTGTGCGCAATTGATATGGTTAAAGATCCTGAAGTA	420
Db	361		420
Qy	421	CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAGAAGCTGTGGATCTTAGGGATCTT	480
Db	421		480
Qy	481	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG	540
Db	481		540
Qy	541	CTGCCAAGCACATATATAATAAATTGGATAGAGCCAAATAATAGTGGTGATTGGGTA	600
Db	541		600
Qy	601	ATAGTTTCTCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG	660
Db	601		660
Qy	661	CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT	720
Db	661		720
Qy	721	GAACAATTAAGTAACTCTGTGTTTTAGAAATATCAGGGCAAGTACATTTTAAAGTGTGTGA	780
Db	721		780
Qy	781	TGTGATGAATACTTCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Db	781		840
Qy	841	ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Db	841		900
Qy	901	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	960
Db	901		960
Qy	961	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA	1020
Db	961		1020

Qy	1021	AAAATTCCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT	1080
Db	1021	AAAATTCCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT	1080
Qy	1081	CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Db	1081	CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Qy	1141	CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTT	1200
Db	1141	CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTT	1200
Qy	1201	CCTCGTGCTGCTCGACTTTGCCTTTCCATTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA	1260
Db	1201	CCTCGTGCTGCTCGACTTTGCCTTTCCATTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA	1260
Qy	1261	GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACAGACACTCTA	1320
Db	1261	GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACAGACACTCTA	1320
Qy	1321	GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1380
Db	1321	GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1380
Qy	1381	AACCCCTATTGGTGTTACTGGATCAAATCCAAATAAGGAACTCCATGCTTAGAGTTGGAG	1440
Db	1381	AACCCCTATTGGTGTTACTGGATCAAATCCAAATAAGGAACTCCATGCTTAGAGTTGGAG	1440
Qy	1441	TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Db	1441	TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Qy	1501	AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCACGCAGGACTGAGTAACAGA	1560
Db	1501	AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCACGCAGGACTGAGTAACAGA	1560
Qy	1561	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620
Db	1561	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620
Qy	1621	CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAAGATTTTCTATGGAGTCACAGACAC	1680
Db	1621	CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAAGATTTTCTATGGAGTCACAGACAC	1680
Qy	1681	TATTGTGTAACATATCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT	1740
Db	1681	TATTGTGTAACATATCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT	1740

Qy	1741	AGAGATGAAGTAGCCAGATGTATTGCTTGGTAAAGATTGGCTCCAATCAAACCTGAA	1800
Db	1741	AGAGATGAAGTAGCCAGATGTATTGCTTGGTAAAGATTGGCTCCAATCAAACCTGAA	1800
Qy	1801	CAGGCTATGGAACCTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTGTGT	1860
Db	1801	CAGGCTATGGAACCTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTGTGT	1860
Qy	1861	CGGTGCTTGGAAAAATATTTAACAGATGACAAACCTTCTCAGTATTTAATTCAGCTAGTA	1920
Db	1861	CGGTGCTTGGAAAAATATTTAACAGATGACAAACCTTCTCAGTATTTAATTCAGCTAGTA	1920
Qy	1921	CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTACTGAAGAAA	1980
Db	1921	CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTACTGAAGAAA	1980
Qy	1981	GCATTGACTAATCAAAGGATTGGGCACCTTTTCTTTTGGCATTAAAACTGAGATGCAC	2040
Db	1981	GCATTGACTAATCAAAGGATTGGGCACCTTTTCTTTTGGCATTAAAACTGAGATGCAC	2040
Qy	2041	AATAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2100
Db	2041	AATAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2100
Qy	2101	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTAACT	2160
Db	2101	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTAACT	2160
Qy	2161	GACATTCTCAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTAGTT	2220
Db	2161	GACATTCTCAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTAGTT	2220
Qy	2221	GAGCAAATGAGGCGACCAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC	2280
Db	2221	GAGCAAATGAGGCGACCAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC	2280
Qy	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTGCAATTATGTCTTCTGCAAAA	2340
Db	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTGCAATTATGTCTTCTGCAAAA	2340
Qy	2341	AGGCCACTGTGGTTGAATTGGGAGAACCAGACATCATGTCAGAGTTACTGTTTCAGAAC	2400
Db	2341	AGGCCACTGTGGTTGAATTGGGAGAACCAGACATCATGTCAGAGTTACTGTTTCAGAAC	2400
Qy	2401	AATGAGATCATCTTTAAAAATGGGGATGATTACGGCAAGATATGCTAACACTTCAAATT	2460
Db	2401	AATGAGATCATCTTTAAAAATGGGGATGATTACGGCAAGATATGCTAACACTTCAAATT	2460
Qy	2461	ATTCGTATTATGGAAAAATATCTGGCAAAATCAAGGCTTGATCTTCGAATGTTACCTTAT	2520

Db	2461		ATTCTGATTATGGAATAATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT	2520
Qy	2521		GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCAGAAATCTCAGACT	2580
Db	2521		GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCAGAAATCTCAGACT	2580
Qy	2581		ATTATGCAAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2640
Db	2581		ATTATGCAAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2640
Qy	2641		CTACATCAGTGGCTCAAAGACAAGAACAAGGAGAAATATATGATGCAGCCATTGACCTG	2700
Db	2641		CTACATCAGTGGCTCAAAGACAAGAACAAGGAGAAATATATGATGCAGCCATTGACCTG	2700
Qy	2701		TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760
Db	2701		TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760
Qy	2761		CACAATAGTAACATCATGGTGAAAGACGATGGACAACCTGTTTCATATAGATTTTGGACAC	2820
Db	2761		CACAATAGTAACATCATGGTGAAAGACGATGGACAACCTGTTTCATATAGATTTTGGACAC	2820
Qy	2821		TTTTTGGATCACAGAAGAAAAAATTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG	2880
Db	2821		TTTTTGGATCACAGAAGAAAAAATTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG	2880
Qy	2881		ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940
Db	2881		ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940
Qy	2941		TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT	3000
Db	2941		TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT	3000
Qy	3001		CTCTTCATAAATCTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060
Db	3001		CTCTTCATAAATCTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060
Qy	3061		GATGACATTGCATACATTGCAAGAGCCCTAGCCTTAGATAAACTGAGCAAGAGGCTTTG	3120
Db	3061		GATGACATTGCATACATTGCAAGAGCCCTAGCCTTAGATAAACTGAGCAAGAGGCTTTG	3120
Qy	3121		GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Db	3121		GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Qy	3181		TGGATCTTCCACACAATTAACACGATGCATTGAACTGAAAGATAACTGAGAAAATGAAA	3240

Db	3181	TGGATCTTCCACACAATTAACAGCATGCACTGAACTGAAAAGATAACTGAGAAAAATGAAA	3240
Qy	3241	GCTCACTCTGGATTCCCACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA	3300
Db	3241	GCTCACTCTGGATTCCCACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA	3300
Qy	3301	TAGGAATTGCACAATCCATGAACAGCATTAGATTACAGCAAGAACAGAAATAAAATACT	3360
Db	3301	TAGGAATTGCACAATCCATGAACAGCATTAGATTACAGCAAGAACAGAAATAAAATACT	3360
Qy	3361	ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAACTAGTTCATTTC	3420
Db	3361	ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAACTAGTTCATTTC	3420
Qy	3421	AAAA 3424	
Db	3421	AAAA 3424	

RESULT 2

ABL59523

ID ABL59523 standard; cDNA; 3424 BP.

XX

AC ABL59523;

XX

DT 11-JUN-2007 (revised)

DT 16-JUL-2002 (first entry)

XX

DE Human phosphatidylinositol-3-kinase catalytic alpha cDNA SEQ ID NO:23.

XX

KW Human; phosphatidylinositol-3-kinase catalytic alpha; enzyme; tumour;

KW lipid associated gene; lipid metabolism; lipid synthesis;

KW chromosome 3q26.3; gene; ss.

XX

OS Homo sapiens.

XX

FN W0200227028-A1.

XX

PD 04-APR-2002.

XX

PF 27-SEP-2001; 2001WO-US030366.

XX

PR 28-SEP-2000; 2000US-00676052.

XX

PA (ATAI-) ATAIRGIN TECHNOLOGIES INC.

XX

PI Skinner MK, Patton JL, Chaudhary J;

XX

DR WPI; 2002-405056/43.

DR PC:NCBI; gi472990.
 DR PC_ENCPRO:NCBI; gi472991.

XX

PT Identifying tumor characteristics in a tissue sample taken from a
 PT patient, involves determining the copy number or expression level of
 PT genes associated with lipid metabolism, synthesis or action.

XX

PS Example 1; Page 82-83; 113pp; English.

XX

CC The present invention describes a method for identifying tumour
 CC characteristics, comprising measuring a copy number or expression level
 CC of at least two genes associated with lipid metabolism, synthesis, or
 CC action in cells from a patient tissue sample, and comparing the results
 CC with a copy number or expression level of the genes in a normal cell.
 CC Also described is an array of nucleic acid polymers immobilised on a
 CC solid support, comprising a solid support, at least two different nucleic
 CC acid polymers which are each specific for a different gene associated
 CC with lipid metabolism, synthesis or action, where each nucleic acid
 CC polymer is located at a predetermined position on the solid support, and
 CC the array comprises nucleic acid polymers which are specific for less
 CC than 100 genes other than the selected genes. The method is useful for
 CC determining tumour characteristics in a tissue sample taken from a
 CC patient. The present sequence represents a human lipid-associated gene
 CC related cDNA sequence, which is used in the exemplification of the
 CC present invention

CC

CC Revised record issued on 11-JUN-2007 : Enhanced with precomputed
 CC information from BOND.

XX

SQ Sequence 3424 BP; 1134 A; 618 C; 709 G; 963 T; 0 U; 0 Other;

Query Match 100.0%; Score 3424; DB 1; Length 3424;
 Best Local Similarity 100.0%;
 Matches 3424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAAGTGTGGGGCATCCACTTGATG 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAAGTGTGGGGCATCCACTTGATG 60

 Qy 61 CCCCCAAGAATCCTAGTGGAAATGTTTACTACCAATGGAATGATAGTGACTTTAGAATGC 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 CCCCCAAGAATCCTAGTGGAAATGTTTACTACCAATGGAATGATAGTGACTTTAGAATGC 120

 Qy 121 CTCCTGTAGGCTACATTAGTAAGTATAAAGCATGAAGTATTAAAGAAGCAAGAAAATAC 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 CTCCTGTAGGCTACATTAGTAAGTATAAAGCATGAAGTATTAAAGAAGCAAGAAAATAC 180

 Qy 181 CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAGAA 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db	181	CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTACCCAGAA	240
Qy	241	GCAGAAAGGGAAGAATTTTTTGTATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAA	300
Db	241	GCAGAAAGGGAAGAATTTTTTGTATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAA	300
Qy	301	CCATTTTTTAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Db	301	CCATTTTTTAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Qy	361	ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTGATATGGTTAAAGATCCTGAAGTA	420
Db	361	ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTGATATGGTTAAAGATCCTGAAGTA	420
Qy	421	CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAGAAGCTGTGGATCTTAGGGATCTT	480
Db	421	CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAGAAGCTGTGGATCTTAGGGATCTT	480
Qy	481	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTACCAGAG	540
Db	481	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTACCAGAG	540
Qy	541	CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTGGGTA	600
Db	541	CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTGGGTA	600
Qy	601	ATAGTTTCTCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG	660
Db	601	ATAGTTTCTCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG	660
Qy	661	CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT	720
Db	661	CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT	720
Qy	721	GAACAATTAAGTCTGTGTTTTAGAAATATCAGGCAAGTACATTTTAAAGTGTGTGGA	780
Db	721	GAACAATTAAGTCTGTGTTTTAGAAATATCAGGCAAGTACATTTTAAAGTGTGTGGA	780
Qy	781	TGTGATGAATACTTCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Db	781	TGTGATGAATACTTCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Qy	841	ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Db	841	ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Qy	901	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	960
Db	901	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	960

Qy	961	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA	1020
Db	961	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA	1020
Qy	1021	AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT	1080
Db	1021	AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT	1080
Qy	1081	CGAACAGGTATCTACCATGGAGGAGAACCCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Db	1081	CGAACAGGTATCTACCATGGAGGAGAACCCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Qy	1141	CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCTGTACTT	1200
Db	1141	CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCTGTACTT	1200
Qy	1201	CCTCGTGTGCTCGACTTTGCCTTTCCATTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA	1260
Db	1201	CCTCGTGTGCTCGACTTTGCCTTTCCATTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA	1260
Qy	1261	GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACAGACACTCTA	1320
Db	1261	GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACAGACACTCTA	1320
Qy	1321	GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1380
Db	1321	GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1380
Qy	1381	AACCCATTGGTGTTACTGGATCAAATCCAAATAAGAACTCCATGCTTAGAGTTGGAG	1440
Db	1381	AACCCATTGGTGTTACTGGATCAAATCCAAATAAGAACTCCATGCTTAGAGTTGGAG	1440
Qy	1441	TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Db	1441	TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Qy	1501	AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Db	1501	AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Qy	1561	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620
Db	1561	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620
Qy	1621	CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAAGATTTTCTATGGAGTCACAGACAC	1680
Db	1621	CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAAGATTTTCTATGGAGTCACAGACAC	1680

Qy	1681	TATTGTGTAACACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT	1740
Db	1681	TATTGTGTAACACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT	1740
Qy	1741	AGAGATGAAGTAGCCAGATGTATTGCTTGGTAAAAGATTGGCTCCAATCAAACCTGAA	1800
Db	1741	AGAGATGAAGTAGCCAGATGTATTGCTTGGTAAAAGATTGGCTCCAATCAAACCTGAA	1800
Qy	1801	CAGGCTATGGAACCTCTGAGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT	1860
Db	1801	CAGGCTATGGAACCTCTGAGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT	1860
Qy	1861	CGGTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTAGCTAGTA	1920
Db	1861	CGGTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTAGCTAGTA	1920
Qy	1921	CAGGTCTTAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTACTGAAGAAA	1980
Db	1921	CAGGTCTTAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTACTGAAGAAA	1980
Qy	1981	GCATTGACTAATCAAAGGATTGGGCACCTTTTCTTTGGCATTTAAATCTGAGATGCAC	2040
Db	1981	GCATTGACTAATCAAAGGATTGGGCACCTTTTCTTTGGCATTTAAATCTGAGATGCAC	2040
Qy	2041	AATAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2100
Db	2041	AATAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2100
Qy	2101	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTAACT	2160
Db	2101	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTAACT	2160
Qy	2161	GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTAGTT	2220
Db	2161	GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTAGTT	2220
Qy	2221	GAGCAATGAGGCGACCAAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC	2280
Db	2221	GAGCAATGAGGCGACCAAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC	2280
Qy	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTGCAATTATGTCTTCTGCAAAA	2340
Db	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTGCAATTATGTCTTCTGCAAAA	2340
Qy	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTGAGAGTTACTGTTTCAGAAC	2400
Db	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTGAGAGTTACTGTTTCAGAAC	2400
Qy	2401	AATGAGATCATCTTTAAAAATGGGGATGATTACGGCAAGATATGCTAACACTTCAAATT	2460

Db	2401	AATGAGATCATCTTTAAAAATGGGGATGATTACGGCAAGATATGCTAACACTTCAAATT	2460	
Qy	2461	ATTTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT	2520	
Db	2461	ATTTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT	2520	
Qy	2521	GGTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCAGAAATCTCAGACT	2580	
Db	2521	GGTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCAGAAATCTCAGACT	2580	
Qy	2581	ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2640	
Db	2581	ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2640	
Qy	2641	CTACATCAGTGGCTCAAAGACAAGAACAAGGAGAAATATATGATGCAGCCATTGACCTG	2700	
Db	2641	CTACATCAGTGGCTCAAAGACAAGAACAAGGAGAAATATATGATGCAGCCATTGACCTG	2700	
Qy	2701	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760	
Db	2701	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760	
Qy	2761	CACAATAGTAACATCATGGTGAAAGACGATGGACAACCTGTTTCATATAGATTTTGGACAC	2820	
Db	2761	CACAATAGTAACATCATGGTGAAAGACGATGGACAACCTGTTTCATATAGATTTTGGACAC	2820	
Qy	2821	TTTTTGGATCACAGAAGAAAAAATTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG	2880	
Db	2821	TTTTTGGATCACAGAAGAAAAAATTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG	2880	
Qy	2881	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940	
Db	2881	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940	
Qy	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT	3000	
Db	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT	3000	
Qy	3001	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060	
Db	3001	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060	
Qy	3061	GATGACATTGCATACATTGAAAGACCCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG	3120	
Db	3061	GATGACATTGCATACATTGAAAGACCCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG	3120	
Qy	3121	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAAACAAAATGGAT	3180	

Db	3121	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAAACAAAAATGGAT	3180
Qy	3181	TGGATCTTCCACACAATTAACAGCATGCATTGAACTGAAAGATAACTGAGAAAAATGAAA	3240
Db	3181	TGGATCTTCCACACAATTAACAGCATGCATTGAACTGAAAGATAACTGAGAAAAATGAAA	3240
Qy	3241	GCTCACTCTGGATTCCCACTGCACTGTTAATAAATCTCAGCAGGCCAAAGACCGATTGCA	3300
Db	3241	GCTCACTCTGGATTCCCACTGCACTGTTAATAAATCTCAGCAGGCCAAAGACCGATTGCA	3300
Qy	3301	TAGGAATTGCACAATCCATGAACAGCATTAGATTACAGCAAGAACAGAAATAAAATACT	3360
Db	3301	TAGGAATTGCACAATCCATGAACAGCATTAGATTACAGCAAGAACAGAAATAAAATACT	3360
Qy	3361	ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAACTAGTTCATTTC	3420
Db	3361	ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAACTAGTTCATTTC	3420
Qy	3421	AAAA 3424	
Db	3421	AAAA 3424	

RESULT 3

ADE85076

ID ADE85076 standard; DNA; 3424 BP.

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AC ADE85076;

XX

DT 11-JUN-2007 (revised)

DT 29-JAN-2004 (first entry)

XX

DE Farnesyl transferase inhibitor modulated leukemia associated gene #295.

XX

KW ss; cytostatic; farnesyl transferase inhibitor; gene expression;
quinolinone; leukemia; cancer.

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OS Homo sapiens.

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PN WO2003038129-A2.

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PD 08-MAY-2003.

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PF 30-OCT-2002; 2002WO-US034784.

XX

PR 30-OCT-2001; 2001US-0338997P.

PR 30-OCT-2001; 2001US-0340081P.

PR 30-OCT-2001; 2001US-0340938P.

PR 30-OCT-2001; 2001US-0341012P.

XX
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
XX
PI Raponi M;
XX
DR WPI; 2003-513497/48.
DR PC:NCBI; gi472990.
DR PC_ENCPRO:NCBI; gi472991.
XX
PT Determining whether a patient will respond to treatment with a farnesyl
PT transferase inhibitor, by analyzing the expression of gene that is
PT differentially modulated in the presence of the inhibitor.
XX
PS Disclosure; SEQ ID NO 295; 346pp; English.
XX
CC The invention relates to a method of determining whether a patient will
CC respond to treatment with a farnesyl transferase inhibitor (FTI), by
CC analyzing the expression of gene that is differentially modulated in the
CC presence of an FTI. The method is useful for determining whether a
CC patient will respond to treatment with a FTI such as (B)-6-[amino(4-
CC chlorophenyl)(1-methyl-1H-imidazol-5-yl)methyl]-4-(3-chlorophenyl)-1-
CC methyl-2-(1H)quinolinone, monitoring the therapy of a patient, treating a
CC patient with leukemia with FTI if the analysis indicates that the patient
CC will respond. This sequence corresponds to a gene whose expression may be
CC modulated in the presence of FTI.
CC
CC Revised record issued on 11-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 3424 BP; 1134 A; 618 C; 709 G; 963 T; 0 U; 0 Other;

Query Match 100.0%; Score 3424; DB 2; Length 3424;
Best Local Similarity 100.0%;
Matches 3424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAAGTGTGGGGCATCCACTTGATG 60
|||||
Db 1 AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAAGTGTGGGGCATCCACTTGATG 60

Qy 61 CCCCCAAGAATCCTAGTGGAAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAAATGC 120
|||||
Db 61 CCCCCAAGAATCCTAGTGGAAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAAATGC 120

Qy 121 CTCCTGTAGGCTACATTAGTAAGTATAAAGCATGAAGTATTAAAGAAGCAAGAAAATAC 180
|||||
Db 121 CTCCTGTAGGCTACATTAGTAAGTATAAAGCATGAAGTATTAAAGAAGCAAGAAAATAC 180

Qy 181 CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA 240
|||||

Db	181	CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTACCCAGAA	240
Qy	241	GCAGAAAGGGAAGAATTTTTTGTATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAA	300
Db	241	GCAGAAAGGGAAGAATTTTTTGTATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAA	300
Qy	301	CCATTTTTTAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Db	301	CCATTTTTTAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Qy	361	ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTGATATGGTTAAAGATCCTGAAGTA	420
Db	361	ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTGATATGGTTAAAGATCCTGAAGTA	420
Qy	421	CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAGAAGCTGTGGATCTTAGGGATCTT	480
Db	421	CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAGAAGCTGTGGATCTTAGGGATCTT	480
Qy	481	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTACCAGAG	540
Db	481	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTACCAGAG	540
Qy	541	CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTGGGTA	600
Db	541	CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTGGGTA	600
Qy	601	ATAGTTTCTCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG	660
Db	601	ATAGTTTCTCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG	660
Qy	661	CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAAGTATGTTGCTATCATCT	720
Db	661	CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAAGTATGTTGCTATCATCT	720
Qy	721	GAACAATTAAGTCTGTGTTTTAGAAATATCAGGCAAGTACATTTTAAAGTGTGTGGA	780
Db	721	GAACAATTAAGTCTGTGTTTTAGAAATATCAGGCAAGTACATTTTAAAGTGTGTGGA	780
Qy	781	TGTGATGAATACTTCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Db	781	TGTGATGAATACTTCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Qy	841	ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Db	841	ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Qy	901	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	960
Db	901	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	960

Qy	961	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAAATAGAGCACTCAGAATA	1020
Db	961	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAAATAGAGCACTCAGAATA	1020
Qy	1021	AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT	1080
Db	1021	AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT	1080
Qy	1081	CGAACAGGTATCTACCATGGAGGAGAACCCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Db	1081	CGAACAGGTATCTACCATGGAGGAGAACCCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Qy	1141	CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCTGATCTT	1200
Db	1141	CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCTGATCTT	1200
Qy	1201	CCTCGTGTGCTCGACTTTGCCTTTCCATTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA	1260
Db	1201	CCTCGTGTGCTCGACTTTGCCTTTCCATTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA	1260
Qy	1261	GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACAGACACTCTA	1320
Db	1261	GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACAGACACTCTA	1320
Qy	1321	GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1380
Db	1321	GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1380
Qy	1381	AACCCATTGGTGTTACTGGATCAAATCCAAATAAGAACTCCATGCTTAGAGTTGGAG	1440
Db	1381	AACCCATTGGTGTTACTGGATCAAATCCAAATAAGAACTCCATGCTTAGAGTTGGAG	1440
Qy	1441	TTTGACTGGTTTCAGCAGTGTGGTAAAGTTCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Db	1441	TTTGACTGGTTTCAGCAGTGTGGTAAAGTTCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Qy	1501	AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCACGCAGGACTGAGTAACAGA	1560
Db	1501	AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCACGCAGGACTGAGTAACAGA	1560
Qy	1561	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620
Db	1561	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620
Qy	1621	CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAAGATTTTCTATGGAGTCACAGACAC	1680
Db	1621	CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAAGATTTTCTATGGAGTCACAGACAC	1680

Qy	1681	TATTGTGTAACACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTAAATGGAATTCT	1740
Db	1681	TATTGTGTAACACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTAAATGGAATTCT	1740
Qy	1741	AGAGATGAAGTAGCCAGATGTATTGCTTGGTAAAAGATTGGCTCCAATCAAACCTGAA	1800
Db	1741	AGAGATGAAGTAGCCAGATGTATTGCTTGGTAAAAGATTGGCTCCAATCAAACCTGAA	1800
Qy	1801	CAGGCTATGGAACCTCTGAGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT	1860
Db	1801	CAGGCTATGGAACCTCTGAGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT	1860
Qy	1861	CGGTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTAGCTAGTA	1920
Db	1861	CGGTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTAGCTAGTA	1920
Qy	1921	CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTACTGAAGAAA	1980
Db	1921	CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTACTGAAGAAA	1980
Qy	1981	GCATTGACTAATCAAAGGATTGGGCACCTTTTCTTTGGCATTTAAAATCTGAGATGCAC	2040
Db	1981	GCATTGACTAATCAAAGGATTGGGCACCTTTTCTTTGGCATTTAAAATCTGAGATGCAC	2040
Qy	2041	AATAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2100
Db	2041	AATAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2100
Qy	2101	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTAACT	2160
Db	2101	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTAACT	2160
Qy	2161	GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTAGTT	2220
Db	2161	GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTAGTT	2220
Qy	2221	GAGCAATGAGGCGACCAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC	2280
Db	2221	GAGCAATGAGGCGACCAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC	2280
Qy	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTGCAATTATGTCTTCTGCAAAA	2340
Db	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTGCAATTATGTCTTCTGCAAAA	2340
Qy	2341	AGGCCACTGTGGTTGAATTGGGAGAACCAGACATCATGTCAGAGTTACTGTTTCAGAAC	2400
Db	2341	AGGCCACTGTGGTTGAATTGGGAGAACCAGACATCATGTCAGAGTTACTGTTTCAGAAC	2400
Qy	2401	AATGAGATCATCTTTAAAAATGGGGATGATTACGGCAAGATATGCTAACACTTCAAATT	2460

Db	2401	AATGAGATCATCTTTAAAAATGGGGATGATTACGGCAAGATATGCTAACACTTCAAATT	2460	
Qy	2461	ATTTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT	2520	
Db	2461	ATTTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT	2520	
Qy	2521	GGTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCAGAAATCTCAGACT	2580	
Db	2521	GGTGTCTGTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCAGAAATCTCAGACT	2580	
Qy	2581	ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2640	
Db	2581	ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2640	
Qy	2641	CTACATCAGTGGCTCAAAGACAAGAACAAGGAGAAATATATGATGCAGCCATTGACCTG	2700	
Db	2641	CTACATCAGTGGCTCAAAGACAAGAACAAGGAGAAATATATGATGCAGCCATTGACCTG	2700	
Qy	2701	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760	
Db	2701	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760	
Qy	2761	CACAATAGTAACATCATGGTGAAAGACGATGGACAACCTGTTTCATATAGATTTTGGACAC	2820	
Db	2761	CACAATAGTAACATCATGGTGAAAGACGATGGACAACCTGTTTCATATAGATTTTGGACAC	2820	
Qy	2821	TTTTTGGATCACAGAAGAAAAAATTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG	2880	
Db	2821	TTTTTGGATCACAGAAGAAAAAATTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG	2880	
Qy	2881	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940	
Db	2881	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940	
Qy	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT	3000	
Db	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT	3000	
Qy	3001	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060	
Db	3001	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060	
Qy	3061	GATGACATTGCATACATTGAAAGACCCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG	3120	
Db	3061	GATGACATTGCATACATTGAAAGACCCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG	3120	
Qy	3121	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAAACAAAATGGAT	3180	

Db	3121	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAAACAAAAATGGAT	3180
Qy	3181	TGGATCTTCCACACAATTAACAGCATGCATTGAACTGAAAGATAACTGAGAAAAATGAAA	3240
Db	3181	TGGATCTTCCACACAATTAACAGCATGCATTGAACTGAAAGATAACTGAGAAAAATGAAA	3240
Qy	3241	GCTCACTCTGGATTCCCACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA	3300
Db	3241	GCTCACTCTGGATTCCCACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA	3300
Qy	3301	TAGGAATTGCACAATCCATGAACAGCATTAGATTACAGCAAGAACAGAAATAAAATACT	3360
Db	3301	TAGGAATTGCACAATCCATGAACAGCATTAGATTACAGCAAGAACAGAAATAAAATACT	3360
Qy	3361	ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAACTAGTTCATTTC	3420
Db	3361	ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAACTAGTTCATTTC	3420
Qy	3421	AAAA 3424	
Db	3421	AAAA 3424	

RESULT 4

ADZ00490

ID ADZ00490 standard; cDNA; 3424 BP.

XX

AC ADZ00490;

XX

DT 11-JUN-2007 (revised)

DT 16-JUN-2005 (first entry)

XX

DE p110-beta coding sequence.

XX

KW ss; Anorectic; Antidiabetic; p110-beta; phosphoinositide 3-kinase; p85;

KW ras; insulin resistance; obesity; gene.

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OS Homo sapiens.

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FH	Key	Location/Qualifiers
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FT	CDS	13..3219
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FT		/*tag= a
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PN WO2005031341-A2.

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PD 07-APR-2005.

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PF 28-SEP-2004; 2004WO-IB003926.

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PR 29-SEP-2003; 2003US-0507226P.
 PR 13-JUL-2004; 2004US-0587333P.

XX
 PA (PFIZ) PFIZER HEALTH AB.
 XX

PI Bougneres P;
 XX

DR WPI; 2005-273421/28.
 DR P-PSDB; ADZ00491.
 DR GENBANK; Z29090.
 DR PC:NCBI; gi472990.
 DR PC_ENCPRO:NCBI; gi472991.
 XX

PT Predicting a subject's likelihood of developing insulin resistance,
 PT useful for treating insulin resistance and obesity, comprises determining
 PT in a subject the identity of an allele at position 100 of a specific
 PT sequence.
 XX

PS Disclosure; SEQ ID NO 2; 88pp; English.
 XX

CC This sequence represents the p110-beta gene. p110-beta is a catalytic
 CC subunit of a phosphoinositide 3-kinase, which also comprises a regulatory
 CC subunit of about 85 kD. The p110 protein comprises a kinase domain at the
 CC C-terminus, and a p85 and ras binding domain at the N-terminus. The
 CC method of the invention for predicting a subject's likelihood of
 CC developing insulin resistance comprises determining in a subject the
 CC identity of the nucleotide present at a position corresponding to
 CC position -359 of the p110-beta gene , where the allele comprising the
 CC nucleotide is correlated with an increased or decreased likelihood of
 CC developing insulin resistance. The method of the invention is useful for
 CC treating obesity and insulin resistance and for assessing and conducting
 CC clinical trials of medicaments.
 CC

CC Revised record issued on 11-JUN-2007 : Enhanced with precomputed
 CC information from BOND.
 XX

SQ Sequence 3424 BP; 1134 A; 618 C; 709 G; 963 T; 0 U; 0 Other;

Query Match 100.0%; Score 3424; DB 4; Length 3424;
 Best Local Similarity 100.0%;
 Matches 3424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAAGTGTGGGGCATCCACTTGATG	60
Db	1	AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAAGTGTGGGGCATCCACTTGATG	60
Qy	61	CCCCCAAGAATCCTAGTGGAAATGTTTACTACCAATGGAATGATAGTGACTTTAGAATGC	120
Db	61	CCCCCAAGAATCCTAGTGGAAATGTTTACTACCAATGGAATGATAGTGACTTTAGAATGC	120

Qy	121	CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC	180
Db	121	CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC	180
Qy	181	CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA	240
Db	181	CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA	240
Qy	241	GCAGAAAGGGAAGAATTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAA	300
Db	241	GCAGAAAGGGAAGAATTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAA	300
Qy	301	CCATTTTTTAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Db	301	CCATTTTTTAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Qy	361	ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA	420
Db	361	ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA	420
Qy	421	CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAGAAGCTGTGGATCTTAGGGATCTT	480
Db	421	CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAGAAGCTGTGGATCTTAGGGATCTT	480
Qy	481	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG	540
Db	481	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG	540
Qy	541	CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTGGGTA	600
Db	541	CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTGGGTA	600
Qy	601	ATAGTTTCTCCAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG	660
Db	601	ATAGTTTCTCCAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG	660
Qy	661	CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT	720
Db	661	CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT	720
Qy	721	GAACAATTAAGTCTGTGTTTTAGAAATATCAGGGCAAGTACATTTTAAAGTGTGTGGA	780
Db	721	GAACAATTAAGTCTGTGTTTTAGAAATATCAGGGCAAGTACATTTTAAAGTGTGTGGA	780
Qy	781	TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Db	781	TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840

Qy	841	ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Db	841	ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Qy	901	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	960
Db	901	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	960
Qy	961	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA	1020
Db	961	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA	1020
Qy	1021	AAAATCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT	1080
Db	1021	AAAATCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT	1080
Qy	1081	CGAACAGGTATCTACCATGGAGGAGAACCCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Db	1081	CGAACAGGTATCTACCATGGAGGAGAACCCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Qy	1141	CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCTGATCTT	1200
Db	1141	CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCTGATCTT	1200
Qy	1201	CCTCGTGTGCTCGACTTTGCCTTTCCATTTGCTCTGTAAAGGCCGAAAGGGTGCTAAA	1260
Db	1201	CCTCGTGTGCTCGACTTTGCCTTTCCATTTGCTCTGTAAAGGCCGAAAGGGTGCTAAA	1260
Qy	1261	GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTGTTGATTACACAGACACTCTA	1320
Db	1261	GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTGTTGATTACACAGACACTCTA	1320
Qy	1321	GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1380
Db	1321	GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1380
Qy	1381	AACCCATTGGTGTTACTGGATCAAATCCAAATAAGAAAGTCCATGCTTAGAGTTGGAG	1440
Db	1381	AACCCATTGGTGTTACTGGATCAAATCCAAATAAGAAAGTCCATGCTTAGAGTTGGAG	1440
Qy	1441	TTTGAAGTGGTTCAGCAGTGTGGTAAAGTTCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Db	1441	TTTGAAGTGGTTCAGCAGTGTGGTAAAGTTCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Qy	1501	AATTGGTCTGTATCCCAGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Db	1501	AATTGGTCTGTATCCCAGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Qy	1561	CTAGCTAGAGACAATGAATTAAGGGAAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620

Db	1561		CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620
Qy	1621		CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAAGATTTTCTATGGAGTCACAGACAC	1680
Db	1621		CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAAGATTTTCTATGGAGTCACAGACAC	1680
Qy	1681		TATTGTGTAACATATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT	1740
Db	1681		TATTGTGTAACATATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT	1740
Qy	1741		AGAGATGAAGTAGCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1800
Db	1741		AGAGATGAAGTAGCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1800
Qy	1801		CAGGCTATGGAACCTCTGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT	1860
Db	1801		CAGGCTATGGAACCTCTGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT	1860
Qy	1861		CGGTGCTTGGA AAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA	1920
Db	1861		CGGTGCTTGGA AAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA	1920
Qy	1921		CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTACTGAAGAAA	1980
Db	1921		CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTACTGAAGAAA	1980
Qy	1981		GCATTGACTAATCAAAGGATTGGGCACTTTTCTTTTGGCATTAAAATCTGAGATGCAC	2040
Db	1981		GCATTGACTAATCAAAGGATTGGGCACTTTTCTTTTGGCATTAAAATCTGAGATGCAC	2040
Qy	2041		AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2100
Db	2041		AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2100
Qy	2101		ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAGAGCTCATTAACCTAACT	2160
Db	2101		ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAGAGCTCATTAACCTAACT	2160
Qy	2161		GACATTCTCAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT	2220
Db	2161		GACATTCTCAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT	2220
Qy	2221		GAGCAATGAGGCGACCAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC	2280
Db	2221		GAGCAATGAGGCGACCAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC	2280
Qy	2281		CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAA	2340

Db	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTGCAATTATGTCTTCTGCAAAA	2340
Qy	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTGAGAGTTACTGTTTCAGAAC	2400
Db	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTGAGAGTTACTGTTTCAGAAC	2400
Qy	2401	AATGAGATCATCTTTAAAAATGGGGATGATTACGGCAAGATATGCTAACACTTCAAATT	2460
Db	2401	AATGAGATCATCTTTAAAAATGGGGATGATTACGGCAAGATATGCTAACACTTCAAATT	2460
Qy	2461	ATTCGTATTATGAAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT	2520
Db	2461	ATTCGTATTATGAAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT	2520
Qy	2521	GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT	2580
Db	2521	GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT	2580
Qy	2581	ATTATGCAAAATTCAGTGCAAAGGCGGCTTGAAGGTGCACTGCAGTTCAACAGCCACACA	2640
Db	2581	ATTATGCAAAATTCAGTGCAAAGGCGGCTTGAAGGTGCACTGCAGTTCAACAGCCACACA	2640
Qy	2641	CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG	2700
Db	2641	CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG	2700
Qy	2701	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760
Db	2701	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760
Qy	2761	CACAATAGTAACATCATGGTGAAAGACGATGGACAACCTGTTTCATATAGATTTTGGACAC	2820
Db	2761	CACAATAGTAACATCATGGTGAAAGACGATGGACAACCTGTTTCATATAGATTTTGGACAC	2820
Qy	2821	TTTTTGGATCACAAGAAGAAAAAATTGGTTATAAACGAGAACGTGTGCCATTGTGTTTG	2880
Db	2821	TTTTTGGATCACAAGAAGAAAAAATTGGTTATAAACGAGAACGTGTGCCATTGTGTTTG	2880
Qy	2881	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940
Db	2881	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940
Qy	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT	3000
Db	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT	3000
Qy	3001	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060
Db	3001	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060

Qy	3061	GATGACATTGCATACATTTCGAAAGACCCCTAGCCTTAGATAAACTGAGCAAGAGGCTTTG	3120
Db	3061	GATGACATTGCATACATTTCGAAAGACCCCTAGCCTTAGATAAACTGAGCAAGAGGCTTTG	3120
Qy	3121	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Db	3121	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Qy	3181	TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA	3240
Db	3181	TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA	3240
Qy	3241	GCTCACTCTGGATTCCCACTGCACTGTTAATAACTCTCAGCAGGCAAGACCGATTGCA	3300
Db	3241	GCTCACTCTGGATTCCCACTGCACTGTTAATAACTCTCAGCAGGCAAGACCGATTGCA	3300
Qy	3301	TAGGAATTGCACAATCCATGAACAGCATTAGATTACAGCAAGAACGAAATAAAATACT	3360
Db	3301	TAGGAATTGCACAATCCATGAACAGCATTAGATTACAGCAAGAACGAAATAAAATACT	3360
Qy	3361	ATATAATTTAAATAATGTAAACGCAAAACAGGGTTTGATAGCACTTAACTAGTTCATTTT	3420
Db	3361	ATATAATTTAAATAATGTAAACGCAAAACAGGGTTTGATAGCACTTAACTAGTTCATTTT	3420
Qy	3421	AAAA 3424	
Db	3421	AAAA 3424	

RESULT 5

AEH10445

ID AEH10445 standard; cDNA; 3424 BP.

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AC AEH10445;

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DT 11-JUN-2007 (revised)

DT 01-JUN-2006 (first entry)

XX

DE PIK3CA cDNA SEQ ID 831.

XX

KW gene expression; prognosis; diagnosis; DNA microarray;

KW colorectal disease; colon tumor; colorectal tumor; cytostatic;

KW gastrointestinal disease; neoplasm; ss.

XX

OS Unidentified.

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PN W02005054508-A2.

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PD 16-JUN-2005.

XX
PF 01-DEC-2004; 2004WO-IB004323.

XX
PR 01-DEC-2003; 2003US-0525987P.

PR 01-DEC-2004; 2004US-00000688.

XX
PA (IPSO-) IPSOGEN.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (PAOL-) INST PAOLI CALMETTES IPC.

XX
PI Bertucci F, Houlgatte R, Birnbaum D, Debono S;

XX
DR WPI; 2005-435408/44.
DR PC:NCBI; gi472990.

XX
PT Analyzing differential gene expression associated with histopathologic
PT features of colorectal disease, involves detecting overexpression or
PT underexpression of pool of polynucleotide sequences in colon tissues.

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PS Claim 1; SEQ ID NO 831; 154pp; English.

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CC The invention describes a method of analyzing (M1) differential gene
CC expression associated with histopathologic features of colorectal
CC disease, comprising detecting overexpression or underexpression of a pool
CC of polynucleotide sequences in colon tissues, the pool selected in each
CC of predefined polynucleotide sequence sets chosen from any one of 644
CC sequence sets comprising combinations of SEQ ID No. 1-1596, fully defined
CC in the specification. Also described are: a polynucleotide library (I)
CC useful for the molecular characterization of a colon cancer, comprising
CC or corresponding to a pool of polynucleotide sequences either
CC overexpressed or underexpressed in colon tissue, the pool corresponding
CC to all or part of the polynucleotide sequence chosen from PS1; and
CC assigning (M2) a therapeutic regimen to patient with histopathological
CC features of colorectal disease, e.g. colon cancer, comprising classifying
CC the patient having a poor prognosis or a good prognosis on the basis of
CC (M1), assigning the patient a therapeutic regimen, the therapeutic
CC regiment comprising no adjuvant chemotherapy if the patient is lymph node
CC negative and is classified as having a good prognosis or comprising
CC chemotherapy if the patient has any other combination of lymph node
CC status and expression profile. (M1) is useful for analyzing differential
CC gene expression associated with histopathologic features of colorectal
CC disease. (M1) is useful for analyzing differential gene expression
CC associated with colon tumors, visceral metastases in colon cancer, lymph
CC node metastases in colon cancer, MSI phenotype in colon cancer, location
CC of primary colorectal carcinoma, in colon cancer, and survival and death
CC of patient in colon cancer, where the analysis comprises detection of
CC overexpression or underexpression of pool of polynucleotide sequences in
CC colon tissue, the pool corresponding to specific combination of

Qy	361	ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTGATATGGTTAAAGATCCTGAAGTA	420
Db	361	ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTGATATGGTTAAAGATCCTGAAGTA	420
Qy	421	CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAGAAGCTGTGGATCTTAGGGATCTT	480
Db	421	CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAGAAGCTGTGGATCTTAGGGATCTT	480
Qy	481	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG	540
Db	481	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG	540
Qy	541	CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTGGGTA	600
Db	541	CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTGGGTA	600
Qy	601	ATAGTTTCTCCAATAATGACAAGCAGAAGTATACTCTGAAATCAACCATGACTGTGTG	660
Db	601	ATAGTTTCTCCAATAATGACAAGCAGAAGTATACTCTGAAATCAACCATGACTGTGTG	660
Qy	661	CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT	720
Db	661	CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT	720
Qy	721	GAACAATTAAGTCTGTGTTTTAGAAATATCAGGGCAAGTACATTTTAAAGTGTGTGGA	780
Db	721	GAACAATTAAGTCTGTGTTTTAGAAATATCAGGGCAAGTACATTTTAAAGTGTGTGGA	780
Qy	781	TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Db	781	TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Qy	841	ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Db	841	ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Qy	901	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	960
Db	901	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	960
Qy	961	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA	1020
Db	961	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA	1020
Qy	1021	AAAATTCCTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT	1080
Db	1021	AAAATTCCTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT	1080
Qy	1081	CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140

Db	1081		CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Qy	1141		CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCTGATCTT	1200
Db	1141		CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCTGATCTT	1200
Qy	1201		CCTCGTGTGCTGCAGCTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA	1260
Db	1201		CCTCGTGTGCTGCAGCTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA	1260
Qy	1261		GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTGTTGATTACAGACACTCTA	1320
Db	1261		GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTGTTGATTACAGACACTCTA	1320
Qy	1321		GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTGCTG	1380
Db	1321		GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTGCTG	1380
Qy	1381		AACCTTATTGGTGTACTGGATCAAATCCAAATAAGAACTCCATGCTTAGAGTTGGAG	1440
Db	1381		AACCTTATTGGTGTACTGGATCAAATCCAAATAAGAACTCCATGCTTAGAGTTGGAG	1440
Qy	1441		TTTGAAGTGTTCAGCAGTGTGGTAAAGTTCCAGATATGTGAGTATTGAAGAGCATGCC	1500
Db	1441		TTTGAAGTGTTCAGCAGTGTGGTAAAGTTCCAGATATGTGAGTATTGAAGAGCATGCC	1500
Qy	1501		AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Db	1501		AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Qy	1561		CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620
Db	1561		CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620
Qy	1621		CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC	1680
Db	1621		CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC	1680
Qy	1681		TATTGTGTAACATATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT	1740
Db	1681		TATTGTGTAACATATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT	1740
Qy	1741		AGAGATGAAGTAGCCAGATGTATTGCTTGGTAAAAGATTGGCTCCAATCAAACCTGAA	1800
Db	1741		AGAGATGAAGTAGCCAGATGTATTGCTTGGTAAAAGATTGGCTCCAATCAAACCTGAA	1800
Qy	1801		CAGGCTATGGAACCTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTGTCTGTT	1860

Db	1801	CAGGCTATGGAACCTCTGGACTGTAATTACCCAGATCCTATGGTTTCGAGGTTTTGTGT	1860
Qy	1861	CGGTGCTTGGAAAAATATTTAACAGATGACAAACCTTCTCAGTATTTAATTCAGCTAGTA	1920
Db	1861	CGGTGCTTGGAAAAATATTTAACAGATGACAAACCTTCTCAGTATTTAATTCAGCTAGTA	1920
Qy	1921	CAGGTCCTAAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTACTGAAGAAA	1980
Db	1921	CAGGTCCTAAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTACTGAAGAAA	1980
Qy	1981	GCATTGACTAATCAAAGGATTGGGCACTTTTCTTTTGGCATTAAAACTGAGATGCAC	2040
Db	1981	GCATTGACTAATCAAAGGATTGGGCACTTTTCTTTTGGCATTAAAACTGAGATGCAC	2040
Qy	2041	AATAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTCATGTGGG	2100
Db	2041	AATAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTCATGTGGG	2100
Qy	2101	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGAAAAAGCTCATTAACCTAACT	2160
Db	2101	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGAAAAAGCTCATTAACCTAACT	2160
Qy	2161	GACATTCTCAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTAGTT	2220
Db	2161	GACATTCTCAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTAGTT	2220
Qy	2221	GAGCAATGAGGCGACCAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC	2280
Db	2221	GAGCAATGAGGCGACCAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC	2280
Qy	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTGCAATTATGTCTTCTGCAAAA	2340
Db	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTGCAATTATGTCTTCTGCAAAA	2340
Qy	2341	AGGCCACTGTGGTTGAATTGGGAGAACCAGACATCATGTGAGATTACTGTTTCAGAAC	2400
Db	2341	AGGCCACTGTGGTTGAATTGGGAGAACCAGACATCATGTGAGATTACTGTTTCAGAAC	2400
Qy	2401	AATGAGATCATCTTTAAAAATGGGGATGATTACGGCAAGATATGCTAACACTTCAAATT	2460
Db	2401	AATGAGATCATCTTTAAAAATGGGGATGATTACGGCAAGATATGCTAACACTTCAAATT	2460
Qy	2461	ATTCGTATTATGAAAAATATCTGGCAAAATCAAGGCTTGATCTTCGAATGTTACCTTAT	2520
Db	2461	ATTCGTATTATGAAAAATATCTGGCAAAATCAAGGCTTGATCTTCGAATGTTACCTTAT	2520
Qy	2521	GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT	2580
Db	2521	GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT	2580

Qy	2581	ATTATGCAAAATTCAGTGCAAAGGCGGCTTGAAGGTGCACTGCAGTTCAACAGCCACACA	2640
Db	2581	ATTATGCAAAATTCAGTGCAAAGGCGGCTTGAAGGTGCACTGCAGTTCAACAGCCACACA	2640
Qy	2641	CTACATCAGTGGCTCAAAGACAAGAACAAGGAGAAATATATGATGCAGCCATTGACCTG	2700
Db	2641	CTACATCAGTGGCTCAAAGACAAGAACAAGGAGAAATATATGATGCAGCCATTGACCTG	2700
Qy	2701	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760
Db	2701	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760
Qy	2761	CACAATAGTAACATCATGGTGAAAGACGATGGACAACCTGTTTCATATAGATTTTGGACAC	2820
Db	2761	CACAATAGTAACATCATGGTGAAAGACGATGGACAACCTGTTTCATATAGATTTTGGACAC	2820
Qy	2821	TTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAAGCAGACGTGTGCCATTGTGTTTG	2880
Db	2821	TTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAAGCAGACGTGTGCCATTGTGTTTG	2880
Qy	2881	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940
Db	2881	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940
Qy	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT	3000
Db	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT	3000
Qy	3001	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060
Db	3001	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060
Qy	3061	GATGACATTGCATACATTGAAAAGACCTAGCCTTAGATAAACTGAGCAAGAGGCTTTG	3120
Db	3061	GATGACATTGCATACATTGAAAAGACCTAGCCTTAGATAAACTGAGCAAGAGGCTTTG	3120
Qy	3121	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAATGGAT	3180
Db	3121	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAATGGAT	3180
Qy	3181	TGGATCTTCCACACAATTAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA	3240
Db	3181	TGGATCTTCCACACAATTAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA	3240
Qy	3241	GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAGACCGATTGCA	3300
Db	3241	GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAGACCGATTGCA	3300

Qy 3301 TAGGAATTGCACAATCCATGAACAGCATTAGATTACAGCAAGAACAGAAATAAAATACT 3360
 |||
 Db 3301 TAGGAATTGCACAATCCATGAACAGCATTAGATTACAGCAAGAACAGAAATAAAATACT 3360

Qy 3361 ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAACTAGTTCATTTTC 3420
 |||
 Db 3361 ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAACTAGTTCATTTTC 3420

Qy 3421 AAAA 3424
 |||
 Db 3421 AAAA 3424

RESULT 6

AED31618

ID AED31618 standard; cDNA; 3424 BP.

XX

AC AED31618;

XX

DT 15-DEC-2005 (first entry)

XX

DE cDNA (SEQ ID No:2) encoding human phosphatidylinositol 3-kinase (PIK3CA).

XX

KW cancer; neoplasm; phosphatidylinositol 3-kinase; PIK3CA; tumor;

KW chemotherapy; cytostatic; RNA interference; gene silencing;

KW antisense therapy; gene; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 13..3219

FT /*tag= a

FT /product= "PIK3CA"

XX

PN W02005091849-A2.

XX

PD 06-OCT-2005.

XX

PF 18-FEB-2005; 2005W0-US005193.

XX

PR 02-MAR-2004; 2004US-0548886P.

XX

PA (UYJO) UNIV JOHNS HOPKINS.

XX

PI Samuels Y, Velculescu V, Kinzler KW, Vogelstein B;

XX

DR WPI; 2005-713721/73.

DR P-PSDB; AED31619.

XX

PT Assessing cancer in a human suspected of having cancer, by determining a
 PT non-synonymous, intragenic mutation in a phosphatidylinositol 3-kinase
 PT (PIK3CA) coding sequence in the body sample from a human.

XX
 PS Claim 1; SEQ ID NO 2; 107pp; English.

XX
 CC The invention relates to a method of assessing cancer in a body sample of
 CC a human suspected of having cancer. The method comprises determining a
 CC non-synonymous, intragenic mutation in a phosphatidylinositol 3-kinase
 CC (PIK3CA) coding sequence in the body sample, and identifying the human as
 CC likely to have cancer if a non-synonymous, intragenic mutation in PIK3CA
 CC coding sequence is determined in the body sample. Also described are: (1)
 CC a method of inhibiting progression of a tumor in a human; (2) a method of
 CC identifying candidate chemotherapeutic agents; (3) a method for
 CC delivering an appropriate chemotherapeutic drug to a patient in need; and
 CC (4) a set of one or more primers for amplifying and/or sequencing PIK3CA,
 CC the primers selected from forward primers, reverse primers, or sequencing
 CC primers, where the forward primers are selected from sequences given as
 CC SEQ ID NOs 6-165, the reverse primers are selected from sequences given
 CC as SEQ ID NOs 166-325, and the sequencing primers are selected sequences
 CC given as SEQ ID NOs 326-485 in the specification. The method of the
 CC invention is useful for assessing cancer in a body sample of a human
 CC suspected of having cancer, inhibiting progression of a tumor in a human,
 CC identifying candidate chemotherapeutic agents, and delivering an
 CC appropriate chemotherapeutic drug to a patient in need. This sequence
 CC encodes human PIK3CA.

XX
 SQ Sequence 3424 BP; 1134 A; 618 C; 709 G; 963 T; 0 U; 0 Other;

Query Match 100.0%; Score 3424; DB 4; Length 3424;
 Best Local Similarity 100.0%;
 Matches 3424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAAGTGTGGGGCATCCACTTGATG	60
Db	1	AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAAGTGTGGGGCATCCACTTGATG	60
Qy	61	CCCCAAGAATCCTAGTGAATGTTTACTACCAATGGAATGATAGTGACTTTAGAATGC	120
Db	61	CCCCAAGAATCCTAGTGAATGTTTACTACCAATGGAATGATAGTGACTTTAGAATGC	120
Qy	121	CTCCGTGAGGCTACATTAGTAAGTATAAAGCATGAAGTATTTAAAGAAGCAAGAAAATAC	180
Db	121	CTCCGTGAGGCTACATTAGTAAGTATAAAGCATGAAGTATTTAAAGAAGCAAGAAAATAC	180
Qy	181	CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA	240
Db	181	CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA	240

Qy	241	GCAGAAAGGGAAGAAATTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAA	300
Db	241	GCAGAAAGGGAAGAAATTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAA	300
Qy	301	CCATTTTTTAAAGTAATTGAACCAAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Db	301	CCATTTTTTAAAGTAATTGAACCAAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Qy	361	ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA	420
Db	361	ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA	420
Qy	421	CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAGAAGCTGTGGATCTTAGGGATCTT	480
Db	421	CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAGAAGCTGTGGATCTTAGGGATCTT	480
Qy	481	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG	540
Db	481	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG	540
Qy	541	CTGCCAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTGGGTA	600
Db	541	CTGCCAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTGGGTA	600
Qy	601	ATAGTTTCTCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG	660
Db	601	ATAGTTTCTCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG	660
Qy	661	CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT	720
Db	661	CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT	720
Qy	721	GAACAATTAAGTCTGTGTTTTAGAAATATCAGGCAAGTACATTTTAAAGTGTGTGGA	780
Db	721	GAACAATTAAGTCTGTGTTTTAGAAATATCAGGCAAGTACATTTTAAAGTGTGTGGA	780
Qy	781	TGTGATGAATACTTCCTAGAAAAATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Db	781	TGTGATGAATACTTCCTAGAAAAATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Qy	841	ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Db	841	ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Qy	901	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	960
Db	901	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	960
Qy	961	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTATATAATAGAGCACTCAGAATA	1020

Db	961		TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA	1020
Qy	1021		AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT	1080
Db	1021		AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT	1080
Qy	1081		CGAACAGGTATCTACCATGGAGGAGAACCCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Db	1081		CGAACAGGTATCTACCATGGAGGAGAACCCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Qy	1141		CCTTGTTCGAATCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTT	1200
Db	1141		CCTTGTTCGAATCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTT	1200
Qy	1201		CCTCGTGTGCTCGACTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA	1260
Db	1201		CCTCGTGTGCTCGACTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA	1260
Qy	1261		GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACAGACACTCTA	1320
Db	1261		GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACAGACACTCTA	1320
Qy	1321		GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1380
Db	1321		GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1380
Qy	1381		AACCCATTTGGTGTTACTGGATCAAATCCAAATAAGAAACTCCATGCTTAGAGTTGGAG	1440
Db	1381		AACCCATTTGGTGTTACTGGATCAAATCCAAATAAGAAACTCCATGCTTAGAGTTGGAG	1440
Qy	1441		TTTGACTGGTTTCAGCAGTGTGGTAAAGTTCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Db	1441		TTTGACTGGTTTCAGCAGTGTGGTAAAGTTCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Qy	1501		AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Db	1501		AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Qy	1561		CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620
Db	1561		CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620
Qy	1621		CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC	1680
Db	1621		CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC	1680
Qy	1681		TATTGTGTAACATATCCCGAAATTTACCCAAATTGCTTCTGTCTGTTAAATGGAATTTCT	1740

Db	1681	TATTGTGTAAC TATCCCCGAAATTCACCCAAAT TGCTTCTGTCTGTAAATGGAATTCT	1740
Qy	1741	AGAGATGAAGTAGCC CAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1800
Db	1741	AGAGATGAAGTAGCC CAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1800
Qy	1801	CAGGCTATGGAAC TCTCGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT	1860
Db	1801	CAGGCTATGGAAC TCTCGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT	1860
Qy	1861	CGGTGCTTGGAAAAATATTTAACAGATGACAAAC TTTCTCAGATTTTAATTCAGCTAGTA	1920
Db	1861	CGGTGCTTGGAAAAATATTTAACAGATGACAAAC TTTCTCAGATTTTAATTCAGCTAGTA	1920
Qy	1921	CAGGTCCTAAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTACTGAAGAAA	1980
Db	1921	CAGGTCCTAAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTACTGAAGAAA	1980
Qy	1981	GCATTGACTAATCAAAGGATTGGGCAC TTTTCTTTTGGCATTTAAATCTGAGATGCAC	2040
Db	1981	GCATTGACTAATCAAAGGATTGGGCAC TTTTCTTTTGGCATTTAAATCTGAGATGCAC	2040
Qy	2041	AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2100
Db	2041	AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2100
Qy	2101	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATG GAAAAGCTCATTAACTTAACT	2160
Db	2101	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATG GAAAAGCTCATTAACTTAACT	2160
Qy	2161	GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT	2220
Db	2161	GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT	2220
Qy	2221	GAGCAAATGAGGCGACCAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC	2280
Db	2221	GAGCAAATGAGGCGACCAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC	2280
Qy	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTGCAATTATGTCTTCTGCAAAA	2340
Db	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTGCAATTATGTCTTCTGCAAAA	2340
Qy	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGT CAGAGTTACTGTTTCAGAAC	2400
Db	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGT CAGAGTTACTGTTTCAGAAC	2400
Qy	2401	AATGAGATCATCTTTAAAAATGGGGATGATTACGGCAAGATATGCTAACACTTCAAATT	2460
Db	2401	AATGAGATCATCTTTAAAAATGGGGATGATTACGGCAAGATATGCTAACACTTCAAATT	2460

Qy	2461	ATTCGTATTATGAAAAATATCTGGCAAAATCAAGGCTTGATCTTCGAATGTTACCTTAT	2520
Db	2461	ATTCGTATTATGAAAAATATCTGGCAAAATCAAGGCTTGATCTTCGAATGTTACCTTAT	2520
Qy	2521	GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT	2580
Db	2521	GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT	2580
Qy	2581	ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2640
Db	2581	ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2640
Qy	2641	CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG	2700
Db	2641	CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG	2700
Qy	2701	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760
Db	2701	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760
Qy	2761	CACAATAGTAACATCATGGTGAAAGACGATGGACAACCTGTTTCATATAGATTTTGGACAC	2820
Db	2761	CACAATAGTAACATCATGGTGAAAGACGATGGACAACCTGTTTCATATAGATTTTGGACAC	2820
Qy	2821	TTTTTGGATCACAGAAGAAAAAATTGGTTATAAAGCAGAACGTGTGCCATTTGTTTTG	2880
Db	2821	TTTTTGGATCACAGAAGAAAAAATTGGTTATAAAGCAGAACGTGTGCCATTTGTTTTG	2880
Qy	2881	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940
Db	2881	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940
Qy	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTTCGACAGCATGCCAAT	3000
Db	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTTCGACAGCATGCCAAT	3000
Qy	3001	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060
Db	3001	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060
Qy	3061	GATGACATTGCATACATTGAAAAGACCTAGCCTTAGATAAACTGAGCAAGAGGCTTTG	3120
Db	3061	GATGACATTGCATACATTGAAAAGACCTAGCCTTAGATAAACTGAGCAAGAGGCTTTG	3120
Qy	3121	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Db	3121	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180

Qy	3181	TGGATCTTCCACACAATTAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA	3240
Db	3181	TGGATCTTCCACACAATTAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA	3240
Qy	3241	GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA	3300
Db	3241	GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA	3300
Qy	3301	TAGGAATTGCACAATCCATGAACAGCATTAGATTACAGCAAGAACAGAAATAAAATACT	3360
Db	3301	TAGGAATTGCACAATCCATGAACAGCATTAGATTACAGCAAGAACAGAAATAAAATACT	3360
Qy	3361	ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAACTAGTTCATTTC	3420
Db	3361	ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAACTAGTTCATTTC	3420
Qy	3421	AAAA	3424
Db	3421	AAAA	3424

RESULT 7

AEG93388

ID AEG93388 standard; cDNA; 3424 BP.

XX

AC AEG93388;

XX

DT 11-JUN-2007 (revised)

DT 01-JUN-2006 (first entry)

XX

DE Human tumor cell cDNA SEQ ID NO:884.

XX

KW Gene expression; tumor; ss.

XX

OS Homo sapiens.

XX

FN WO2006036025-A1.

XX

PD 06-APR-2006.

XX

PF 30-SEP-2005; 2005WO-JP018574.

XX

PR 30-SEP-2004; 2004JP-00286259.

PR 28-FEB-2005; 2005JP-00054475.

PR 28-FEB-2005; 2005JP-00054866.

XX

PA (EISA) EISAI CO LTD.

XX

PI Owa T, Yokoi A, Ozawa Y, Kawai T, Ushijima R;

XX
 DR WPI; 2006-293404/30.
 DR PC:NCBI; gi472990.
 DR PC_ENCPRO:NCBI; gi472991.
 XX
 PT Evaluating sensitivity of a tumor cell to a sulfonamide-containing
 PT compound, comprises comparing the expression of specific genes in tumor
 PT cells before and after administration of the compound.
 XX
 PS Claim 1; SEQ ID NO 884; 1405pp; Japanese.
 XX
 CC The invention relates to a method of evaluating the sensitivity of a
 CC tumor cell to a sulfonamide-containing compound, by comparing the
 CC expression level of genes in tumor cells obtained from cancer patients
 CC before and after administration of the sulfonamide-containing compound
 CC and determining the tumor cell to be sensitive to the sulfonamide-
 CC containing compound, when the expression amount of genes in the cell is
 CC increased compared with the expression amount before administration
 CC and/or when the expression amount of one or more genes is decreased
 CC compared with the expression amount before administration. The invention
 CC also relates to an assay reagent of RNA comprising an oligonucleotide
 CC complementary to an RNA which is the transcription product of a gene, and
 CC an immunoassay reagent containing the antibody with respect to a protein
 CC which is a translation product of the gene. The expression level of the
 CC gene, which is the RNA transcription product, is measured using a DNA
 CC microarray or by quantitative PCR. The expression level of protein, which
 CC is a translation product of the gene, is measured by an immunochemical
 CC method such as enzyme linked immunosorbent assay (ELISA),
 CC radioimmunoassay (RIA) or Western blotting. The method enables evaluation
 CC of the sensitivity of a tumor cell to a sulfonamide-containing compound.
 CC This sequence represents human tumor cell cDNA used in the scope of the
 CC invention.
 CC
 CC Revised record issued on 11-JUN-2007 : Enhanced with precomputed
 CC information from BOND.
 XX
 SQ Sequence 3424 BP; 1134 A; 618 C; 709 G; 963 T; 0 U; 0 Other;

Query Match 100.0%; Score 3424; DB 4; Length 3424;
 Best Local Similarity 100.0%;
 Matches 3424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAAGTGTGGGGCATCCACTTGATG	60
Db	1	AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAAGTGTGGGGCATCCACTTGATG	60
Qy	61	CCCCCAAGAATCCTAGTGGAAATGTTTACTACCAATGGAATGATAGTGACTTTAGAAATGC	120
Db	61	CCCCCAAGAATCCTAGTGGAAATGTTTACTACCAATGGAATGATAGTGACTTTAGAAATGC	120

Qy	121	CTCCGTGAGGCTACATTAGTAAGTATAAAGCATGAACTATTTAAAGAAGCAAGAAAAATAC	180
Db	121	CTCCGTGAGGCTACATTAGTAAGTATAAAGCATGAACTATTTAAAGAAGCAAGAAAAATAC	180
Qy	181	CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA	240
Db	181	CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA	240
Qy	241	GCAGAAAGGGAAGAATTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAA	300
Db	241	GCAGAAAGGGAAGAATTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAA	300
Qy	301	CCATTTTTAAAGTAATTGAACCAAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Db	301	CCATTTTTAAAGTAATTGAACCAAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Qy	361	ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA	420
Db	361	ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA	420
Qy	421	CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAGAAGCTGTGGATCTTAGGGATCTT	480
Db	421	CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAGAAGCTGTGGATCTTAGGGATCTT	480
Qy	481	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG	540
Db	481	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG	540
Qy	541	CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTGGGTA	600
Db	541	CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTGGGTA	600
Qy	601	ATAGTTTCTCCAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG	660
Db	601	ATAGTTTCTCCAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG	660
Qy	661	CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT	720
Db	661	CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT	720
Qy	721	GAACAATTAAGTCTGTGTTTTAGAAATATCAGGGCAAGTACATTTTAAAGTGTGTGGA	780
Db	721	GAACAATTAAGTCTGTGTTTTAGAAATATCAGGGCAAGTACATTTTAAAGTGTGTGGA	780
Qy	781	TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Db	781	TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840

Qy	841	ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Db	841	ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Qy	901	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	960
Db	901	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	960
Qy	961	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA	1020
Db	961	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA	1020
Qy	1021	AAAATCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT	1080
Db	1021	AAAATCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT	1080
Qy	1081	CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Db	1081	CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Qy	1141	CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCTGATCTT	1200
Db	1141	CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCTGATCTT	1200
Qy	1201	CCTCGTGTGCTCGACTTTGCCTTTCCATTTGCTCTGTAAAGGCCGAAAGGGTGCTAAA	1260
Db	1201	CCTCGTGTGCTCGACTTTGCCTTTCCATTTGCTCTGTAAAGGCCGAAAGGGTGCTAAA	1260
Qy	1261	GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTGTTGATTACACAGACACTCTA	1320
Db	1261	GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTGTTGATTACACAGACACTCTA	1320
Qy	1321	GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1380
Db	1321	GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1380
Qy	1381	AACCCATTGGTGTTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAG	1440
Db	1381	AACCCATTGGTGTTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAG	1440
Qy	1441	TTTGAAGTGGTTTCAGCAGTGTGGTAAAGTTCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Db	1441	TTTGAAGTGGTTTCAGCAGTGTGGTAAAGTTCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Qy	1501	AATTGGTCTGTATCCCAGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Db	1501	AATTGGTCTGTATCCCAGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Qy	1561	CTAGCTAGAGACAATGAATTAAGGGAAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620

Db	1561	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620
Qy	1621	CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAAGATTTTCTATGGAGTCACAGACAC	1680
Db	1621	CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAAGATTTTCTATGGAGTCACAGACAC	1680
Qy	1681	TATTGTGTAACATATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT	1740
Db	1681	TATTGTGTAACATATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT	1740
Qy	1741	AGAGATGAAGTAGCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1800
Db	1741	AGAGATGAAGTAGCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1800
Qy	1801	CAGGCTATGGAACCTCTGGAATTAACCCAGATCCTATGGTTCGAGGTTTTGCTGTT	1860
Db	1801	CAGGCTATGGAACCTCTGGAATTAACCCAGATCCTATGGTTCGAGGTTTTGCTGTT	1860
Qy	1861	CGGTGCTTGGAAAAATATTTAACAGATGACAAACCTTCTCAGTATTTAATTCAGCTAGTA	1920
Db	1861	CGGTGCTTGGAAAAATATTTAACAGATGACAAACCTTCTCAGTATTTAATTCAGCTAGTA	1920
Qy	1921	CAGGTCCTAAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTACTGAAGAAA	1980
Db	1921	CAGGTCCTAAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTACTGAAGAAA	1980
Qy	1981	GCATTGACTAATCAAAGGATTGGGCACTTTTCTTTTGGCATTAAAAATCTGAGATGCAC	2040
Db	1981	GCATTGACTAATCAAAGGATTGGGCACTTTTCTTTTGGCATTAAAAATCTGAGATGCAC	2040
Qy	2041	AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2100
Db	2041	AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2100
Qy	2101	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAGAGCTCATTAACCTAACT	2160
Db	2101	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAGAGCTCATTAACCTAACT	2160
Qy	2161	GACATTCTCAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTAGTT	2220
Db	2161	GACATTCTCAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTAGTT	2220
Qy	2221	GAGCAATGAGGCGACCAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC	2280
Db	2221	GAGCAATGAGGCGACCAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC	2280
Qy	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTGCAATTATGTCTTCTGCAAAA	2340

Db	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTGCAATTATGTCTTCTGCAAAA	2340
Qy	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTGAGAGTTACTGTTTCAGAAC	2400
Db	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTGAGAGTTACTGTTTCAGAAC	2400
Qy	2401	AATGAGATCATCTTTAAAAATGGGGATGATTACGGCAAGATATGCTAACACTTCAAATT	2460
Db	2401	AATGAGATCATCTTTAAAAATGGGGATGATTACGGCAAGATATGCTAACACTTCAAATT	2460
Qy	2461	ATTCTGATTATGAAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT	2520
Db	2461	ATTCTGATTATGAAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT	2520
Qy	2521	GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT	2580
Db	2521	GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT	2580
Qy	2581	ATTATGCAAAATTCAGTGCAAAGGCGGCTTGAAGGTGCACTGCAGTTCAACAGCCACACA	2640
Db	2581	ATTATGCAAAATTCAGTGCAAAGGCGGCTTGAAGGTGCACTGCAGTTCAACAGCCACACA	2640
Qy	2641	CTACATCAGTGGCTCAAAGACAAGAACAAGGAGAAATATATGATGCAGCCATTGACCTG	2700
Db	2641	CTACATCAGTGGCTCAAAGACAAGAACAAGGAGAAATATATGATGCAGCCATTGACCTG	2700
Qy	2701	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760
Db	2701	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760
Qy	2761	CACAATAGTAACATCATGGTGAAAGACGATGGACAACCTGTTTCATATAGATTTTGGACAC	2820
Db	2761	CACAATAGTAACATCATGGTGAAAGACGATGGACAACCTGTTTCATATAGATTTTGGACAC	2820
Qy	2821	TTTTTGGATCACAAGAAGAAAAAATTGGTTATAAAGGAGAACGTGTGCCATTGTGTTTG	2880
Db	2821	TTTTTGGATCACAAGAAGAAAAAATTGGTTATAAAGGAGAACGTGTGCCATTGTGTTTG	2880
Qy	2881	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940
Db	2881	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940
Qy	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT	3000
Db	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT	3000
Qy	3001	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060
Db	3001	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060

Qy	3061	GATGACATTGCATACATTTCGAAAGACCCCTAGCCTTAGATAAACTGAGCAAGAGGCTTTG	3120
Db	3061	GATGACATTGCATACATTTCGAAAGACCCCTAGCCTTAGATAAACTGAGCAAGAGGCTTTG	3120
Qy	3121	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Db	3121	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Qy	3181	TGGATCTTCCACACAATTAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA	3240
Db	3181	TGGATCTTCCACACAATTAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA	3240
Qy	3241	GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAGACCGATTGCA	3300
Db	3241	GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAGACCGATTGCA	3300
Qy	3301	TAGGAATTGCACAATCCATGAACAGCATTAGATTACAGCAAGAACGAAATAAAATACT	3360
Db	3301	TAGGAATTGCACAATCCATGAACAGCATTAGATTACAGCAAGAACGAAATAAAATACT	3360
Qy	3361	ATATAATTTAAATAATGTAAACGCAAAACAGGGTTTGATAGCACTTAACTAGTTCATTTT	3420
Db	3361	ATATAATTTAAATAATGTAAACGCAAAACAGGGTTTGATAGCACTTAACTAGTTCATTTT	3420
Qy	3421	AAAA 3424	
Db	3421	AAAA 3424	

RESULT 8

AAQ51156

ID AAQ51156 standard; cDNA; 3412 BP.

XX

AC AAQ51156;

XX

DT 25-MAR-2003 (revised)

DT 12-APR-1994 (first entry)

XX

DE Human p110 cDNA.

XX

KW Phosphoinositide kinase; PI; p85 subunit; screening; agonist; antagonist;
 KW cell proliferation; inhibition; prophylaxis; therapy; platelets;
 KW neutrophil activity; 3-phosphorylated phosphoinositides; ds.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1..3207

FT /*tag= a
 FT /note= "PI3- kinase p110"
 XX
 PN W09321328-A1.
 XX
 PD 28-OCT-1993.
 XX
 PF 13-APR-1993; 93WO-GB000761.
 XX
 PR 13-APR-1992; 92GB-00008135.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Hiles ID, Fry MJ, Dhand R, Waterfield MD, Parker PJ, Otsu M;
 PI Panayotou G, Volinia S, Gout I;
 XX
 DR WPI; 1993-351738/44.
 DR P-PSDB; AAR43342.
 XX
 PT Recombinant polypeptide(s) - with phosphoinositide-3 kinase activity,
 PT useful for controlling cell proliferation.
 XX
 PS Claim 7; Fig 16; 146pp; English.
 XX
 CC Southern blot analysis was performed using a bovine cDNA probe contg. a
 CC fragment of a PI3-kinase-encoding sequence and human cDNA isolated from a
 CC cDNA library constructed from mRNA isolated from the human cell line
 CC KGla. Positive clones were sequenced to give the human PI3 kinase p110
 CC sequence shown. This sequence has 95 percent homology with the bovine
 CC sequence. The domain encoding residues 19- 100 of human p110 is
 CC sufficient to encode the kinase which will associate with the p85 kinase
 CC subunit. The gene may be used to provide a protein with PI3 kinase
 CC activity, and is useful for screening for (ant)agonists of PI3 kinase
 CC activity which could be useful for stimulation or inhibition of cell
 CC proliferation and hence prophylaxis or therapy. Platelet or neutrophil
 CC activity or blood glucose levels can be controlled using the kinase. See
 CC also AAQ51155 and AAQ57522-3. (Updated on 25-MAR-2003 to correct PN
 CC field.) (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 3412 BP; 1128 A; 616 C; 706 G; 962 T; 0 U; 0 Other;

Query Match 99.6%; Score 3412; DB 1; Length 3412;
 Best Local Similarity 100.0%;
 Matches 3412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 ATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATGCCCCAAGAATC 72
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 ATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATGCCCCAAGAATC 60

Qy	73	CTAGTGGAAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGCCTCCGTGAGGCT	132
Db	61	CTAGTGGAAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGCCTCCGTGAGGCT	120
Qy	133	ACATTAGTAACATAAAGCATGAACATATTTAAAGAAGCAAGAAAATACCCTCTCCATCAA	192
Db	121	ACATTAGTAACATAAAGCATGAACATATTTAAAGAAGCAAGAAAATACCCTCTCCATCAA	180
Qy	193	CTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAAGCAGAAAGGGAA	252
Db	181	CTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAAGCAGAAAGGGAA	240
Qy	253	GAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAACCATTTTTAAAA	312
Db	241	GAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAACCATTTTTAAAA	300
Qy	313	GTAATTGAACAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAAATTGGTTTTGCT	372
Db	301	GTAATTGAACAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAAATTGGTTTTGCT	360
Qy	373	ATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTACAGGACTTCCGA	432
Db	361	ATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTACAGGACTTCCGA	420
Qy	433	AGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTTAATTCACCTCAT	492
Db	421	AGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTTAATTCACCTCAT	480
Qy	493	AGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAGCTGCCAAAGCAC	552
Db	481	AGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAGCTGCCAAAGCAC	540
Qy	553	ATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTAATAGTTTCTCCA	612
Db	541	ATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTAATAGTTTCTCCA	600
Qy	613	AATAATGACAAGCAGAAGTATACTCTGAAAAATCAACCATGACTGTGTGCCAGAACAGTA	672
Db	601	AATAATGACAAGCAGAAGTATACTCTGAAAAATCAACCATGACTGTGTGCCAGAACAGTA	660
Qy	673	ATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCTGAACAATTAAAA	732
Db	661	ATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCTGAACAATTAAAA	720
Qy	733	CTCTGTGTTTTAGAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGATGTGATGAATAC	792
Db	721	CTCTGTGTTTTAGAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGATGTGATGAATAC	780
Qy	793	TTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGTATAATGCTTGGG	852

Db	781	 TTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGTATAATGCTTGGG	840
Qy	853	AGGATGCCCAATTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAACTGCCAATGGAC	912
Db	841	 AGGATGCCCAATTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAACTGCCAATGGAC	900
Qy	913	TGTTTTACAATGCCATCTTATTCCAGACGCATTTCACAGCTACACCATATATGAATGGA	972
Db	901	 TGTTTTACAATGCCATCTTATTCCAGACGCATTTCACAGCTACACCATATATGAATGGA	960
Qy	973	GAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATAAAAAATCTTTGT	1032
Db	961	 GAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATAAAAAATCTTTGT	1020
Qy	1033	GCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTTCGAACAGGTATC	1092
Db	1021	 GCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTTCGAACAGGTATC	1080
Qy	1093	TACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTACCTTGTTCCAAT	1152
Db	1081	 TACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTACCTTGTTCCAAT	1140
Qy	1153	CCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCTCTGATCTTCTCGTGTCTGT	1212
Db	1141	 CCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCTCTGATCTTCTCGTGTCTGT	1200
Qy	1213	CGACTTTGCCTTTCCATTGTCTCTGTTAAAGGCCGAAAGGGTGCTAAAGAGGAACACTGT	1272
Db	1201	 CGACTTTGCCTTTCCATTGTCTCTGTTAAAGGCCGAAAGGGTGCTAAAGAGGAACACTGT	1260
Qy	1273	CCATTGGCATGGGGAATATAAACTTGTTTGATTACACAGACACTCTAGTATCTGGAAAA	1332
Db	1261	 CCATTGGCATGGGGAATATAAACTTGTTTGATTACACAGACACTCTAGTATCTGGAAAA	1320
Qy	1333	ATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTGCTGAACCTATTGGT	1392
Db	1321	 ATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTGCTGAACCTATTGGT	1380
Qy	1393	GTTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAGTTTGACTGGTTC	1452
Db	1381	 GTTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAGTTTGACTGGTTC	1440
Qy	1453	AGCAGTGTGGTAAAGTCCCAGATATGTCTAGTGATTGAAGAGCATGCCAATTGGTCTGTA	1512
Db	1441	 AGCAGTGTGGTAAAGTCCCAGATATGTCTAGTGATTGAAGAGCATGCCAATTGGTCTGTA	1500
Qy	1513	TCCCAGAGAAGCAGGATTTAGCTATTTCCACGCAGGACTGAGTAACAGACTAGCTAGAGAC	1572

Db	1501	TCCCAGAGAAGCAGGATTAGCTATTCCCACGCAGGACTGAGTAACAGACTAGCTAGAGAC	1560
Qy	1573	AATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACACGAGATCCTCTC	1632
Db	1561	AATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACACGAGATCCTCTC	1620
Qy	1633	TCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGTGTAAC	1692
Db	1621	TCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGTGTAAC	1680
Qy	1693	ATCCCCGAAATTCACCCAAATTGCTTCTGTCTGTTAAATGGAATTCAGAGATGAAGTA	1752
Db	1681	ATCCCCGAAATTCACCCAAATTGCTTCTGTCTGTTAAATGGAATTCAGAGATGAAGTA	1740
Qy	1753	GCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCTATGGAA	1812
Db	1741	GCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCTATGGAA	1800
Qy	1813	CTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTGTCTGTTCCGTGCTTGGAA	1872
Db	1801	CTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTGTCTGTTCCGTGCTTGGAA	1860
Qy	1873	AAATATTTAACAGATGACAAACTTTTCTCAGTATTTAATTCAGCTAGTACAGGTCCTAAAA	1932
Db	1861	AAATATTTAACAGATGACAAACTTTTCTCAGTATTTAATTCAGCTAGTACAGGTCCTAAAA	1920
Qy	1933	TATGAACAATATTTGGATAACTTGCTTGTGAGATTTTACTGAAGAAAGCATTGACTAAT	1992
Db	1921	TATGAACAATATTTGGATAACTTGCTTGTGAGATTTTACTGAAGAAAGCATTGACTAAT	1980
Qy	1993	CAAAGGATTGGGCACTTTTTCTTTTGGCATTAAAACTCGAGATGCACAATAAACAGTT	2052
Db	1981	CAAAGGATTGGGCACTTTTTCTTTTGGCATTAAAACTCGAGATGCACAATAAACAGTT	2040
Qy	2053	AGCCAGAGGTTTGGCCTGCTTTTGGAGTCTATTGTCTGTCATGTGGGATGTATTTGAAG	2112
Db	2041	AGCCAGAGGTTTGGCCTGCTTTTGGAGTCTATTGTCTGTCATGTGGGATGTATTTGAAG	2100
Qy	2113	CACCTGAATAGGCAAGTCGAGGCAATGGAAGAGCTCATTAACCTTAACGACATTCTCAA	2172
Db	2101	CACCTGAATAGGCAAGTCGAGGCAATGGAAGAGCTCATTAACCTTAACGACATTCTCAA	2160
Qy	2173	CAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTAGTTGAGCAAATGAGG	2232
Db	2161	CAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTAGTTGAGCAAATGAGG	2220
Qy	2233	CGACCAGATTTTCATGGATGCCCTACAGGCGTTGCTGTCTCCTCTAAACCCTGCTCATCAA	2292
Db	2221	CGACCAGATTTTCATGGATGCCCTACAGGCGTTGCTGTCTCCTCTAAACCCTGCTCATCAA	2280

Qy	2293	CTAGGAAACCTCAGGCTTAAAGAGTGTGCAATTATGTCTTCTGCAAAAAGGCCACTGTGG	2352
Db	2281	CTAGGAAACCTCAGGCTTAAAGAGTGTGCAATTATGTCTTCTGCAAAAAGGCCACTGTGG	2340
Qy	2353	TTGAATTGGGAGAACCCAGACATCATGTGAGAGTTACTGTTTCAGAACAAATGAGATCATC	2412
Db	2341	TTGAATTGGGAGAACCCAGACATCATGTGAGAGTTACTGTTTCAGAACAAATGAGATCATC	2400
Qy	2413	TTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATTATTCGTATTATG	2472
Db	2401	TTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATTATTCGTATTATG	2460
Qy	2473	GAAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTATGGTTGTCTGTCA	2532
Db	2461	GAAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTATGGTTGTCTGTCA	2520
Qy	2533	ATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCAGAAATTCACACTATTATGCAAATT	2592
Db	2521	ATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCAGAAATTCACACTATTATGCAAATT	2580
Qy	2593	CAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACACTACATCAGTGG	2652
Db	2581	CAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACACTACATCAGTGG	2640
Qy	2653	CTCAAAGACAAGAACAAGGAGAAATATATGATGCAGCCATTGACCTGTTTACACGTTCA	2712
Db	2641	CTCAAAGACAAGAACAAGGAGAAATATATGATGCAGCCATTGACCTGTTTACACGTTCA	2700
Qy	2713	TGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGTCACAATAGTAAC	2772
Db	2701	TGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGTCACAATAGTAAC	2760
Qy	2773	ATCATGGTGAAAGACGATGGACAACGTGTTTCATATAGATTTTGGACACTTTTGGATCAC	2832
Db	2761	ATCATGGTGAAAGACGATGGACAACGTGTTTCATATAGATTTTGGACACTTTTGGATCAC	2820
Qy	2833	AAGAAGAAAAAATTGGTTATAAACGAGAACGTGTGCCATTGTTTTGACACAGGATTTT	2892
Db	2821	AAGAAGAAAAAATTGGTTATAAACGAGAACGTGTGCCATTGTTTTGACACAGGATTTT	2880
Qy	2893	TTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAATTGAGAGGTTT	2952
Db	2881	TTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAATTGAGAGGTTT	2940
Qy	2953	CAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAATCTCTTCATAAAT	3012
Db	2941	CAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAATCTCTTCATAAAT	3000

Qy	3013	CTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTTGATGACATTGCA	3072
Db	3001	CTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTTGATGACATTGCA	3060
Qy	3073	TACATTCGAAAGACCCTAGCCTTAGATAAACTGAGCAAGAGGCTTTGGAGTATTTTCATG	3132
Db	3061	TACATTCGAAAGACCCTAGCCTTAGATAAACTGAGCAAGAGGCTTTGGAGTATTTTCATG	3120
Qy	3133	AAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGATTGGATCTTCCAC	3192
Db	3121	AAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGATTGGATCTTCCAC	3180
Qy	3193	ACAATTAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAAGCTCACTCTGGA	3252
Db	3181	ACAATTAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAAGCTCACTCTGGA	3240
Qy	3253	TTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCATAGGAATTGCAC	3312
Db	3241	TTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCATAGGAATTGCAC	3300
Qy	3313	AATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACTATATAATTTAAA	3372
Db	3301	AATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACTATATAATTTAAA	3360
Qy	3373	TAATGTAAACGCAAACAGGGTTTGATAGCACTTAACTAGTTCATTTCAAAA	3424
Db	3361	TAATGTAAACGCAAACAGGGTTTGATAGCACTTAACTAGTTCATTTCAAAA	3412

RESULT 9

AED31617

ID AED31617 standard; cDNA; 3412 BP.

XX

AC AED31617;

XX

DT 15-DEC-2005 (first entry)

XX

DE cDNA (SEQ ID No:1) encoding human phosphatidylinositol 3-kinase (PIK3CA).

XX

KW cancer; neoplasm; phosphatidylinositol 3-kinase; PIK3CA; tumor;

KW chemotherapy; cytostatic; RNA interference; gene silencing;

KW antisense therapy; gene; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1..3207

FT /*tag= a

FT /product= "PIK3CA"

XX
 PN WO2005091849-A2.
 XX
 PD 06-OCT-2005.
 XX
 PF 18-FEB-2005; 2005WO-US005193.
 XX
 PR 02-MAR-2004; 2004US-0548886P.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Samuels Y, Velculescu V, Kinzler KW, Vogelstein B;
 XX
 DR WPI; 2005-713721/73.
 DR P-PSDB; AED31619.
 XX
 PT Assessing cancer in a human suspected of having cancer, by determining a
 PT non-synonymous, intragenic mutation in a phosphatidylinositol 3-kinase
 PT (PIK3CA) coding sequence in the body sample from a human.
 XX
 PS Disclosure; SEQ ID NO 1; 107pp; English.
 XX
 CC The invention relates to a method of assessing cancer in a body sample of
 CC a human suspected of having cancer. The method comprises determining a
 CC non-synonymous, intragenic mutation in a phosphatidylinositol 3-kinase
 CC (PIK3CA) coding sequence in the body sample, and identifying the human as
 CC likely to have cancer if a non-synonymous, intragenic mutation in PIK3CA
 CC coding sequence is determined in the body sample. Also described are: (1)
 CC a method of inhibiting progression of a tumor in a human; (2) a method of
 CC identifying candidate chemotherapeutic agents; (3) a method for
 CC delivering an appropriate chemotherapeutic drug to a patient in need; and
 CC (4) a set of one or more primers for amplifying and/or sequencing PIK3CA,
 CC the primers selected from forward primers, reverse primers, or sequencing
 CC primers, where the forward primers are selected from sequences given as
 CC SEQ ID NOs 6-165, the reverse primers are selected from sequences given
 CC as SEQ ID NOs 166-325, and the sequencing primers are selected sequences
 CC given as SEQ ID NOs 326-485 in the specification. The method of the
 CC invention is useful for assessing cancer in a body sample of a human
 CC suspected of having cancer, inhibiting progression of a tumor in a human,
 CC identifying candidate chemotherapeutic agents, and delivering an
 CC appropriate chemotherapeutic drug to a patient in need. This sequence
 CC encodes human PIK3CA.
 XX
 SQ Sequence 3412 BP; 1128 A; 616 C; 706 G; 962 T; 0 U; 0 Other;

Query Match 99.6%; Score 3412; DB 4; Length 3412;
 Best Local Similarity 100.0%;
 Matches 3412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	13	ATGCTCCAAGACCATCATCAGGTGAAGTGTGGGCATCCACTTGATGCCCCAAGAATC	72
Db	1	ATGCTCCAAGACCATCATCAGGTGAAGTGTGGGCATCCACTTGATGCCCCAAGAATC	60
Qy	73	CTAGTGAATGTTTACTACCAAAATGGAATGATAGTGACTTTAGAATGCCTCCGTGAGGCT	132
Db	61	CTAGTGAATGTTTACTACCAAAATGGAATGATAGTGACTTTAGAATGCCTCCGTGAGGCT	120
Qy	133	ACATTAGTAACATAAAAGCATGAACATTTTAAAGAAGCAAGAAAATACCTCTCCATCAA	192
Db	121	ACATTAGTAACATAAAAGCATGAACATTTTAAAGAAGCAAGAAAATACCTCTCCATCAA	180
Qy	193	CTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAAGCAGAAAGGGAA	252
Db	181	CTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAAGCAGAAAGGGAA	240
Qy	253	GAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAACCATTTTTAAAA	312
Db	241	GAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAACCATTTTTAAAA	300
Qy	313	GTAATTGAACCAAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAAATTGGTTTTGCT	372
Db	301	GTAATTGAACCAAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAAATTGGTTTTGCT	360
Qy	373	ATCGGCATGCCAGTGTGCGAATTGATATGGTTAAAGATCCTGAAGTACAGGACTTCCGA	432
Db	361	ATCGGCATGCCAGTGTGCGAATTGATATGGTTAAAGATCCTGAAGTACAGGACTTCCGA	420
Qy	433	AGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTTAATTCACCTCAT	492
Db	421	AGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTTAATTCACCTCAT	480
Qy	493	AGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAGCTGCCAAAGCAC	552
Db	481	AGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAGCTGCCAAAGCAC	540
Qy	553	ATATATAATAAAATTGGATAGAGGCCAAATAATAGTGGTGATTGGGTAATAGTTTCTCCA	612
Db	541	ATATATAATAAAATTGGATAGAGGCCAAATAATAGTGGTGATTGGGTAATAGTTTCTCCA	600
Qy	613	AATAATGACAAGCAGAAGTATACTCTGAAAAATCAACCATGACTGTGTGCCAGAACAGTA	672
Db	601	AATAATGACAAGCAGAAGTATACTCTGAAAAATCAACCATGACTGTGTGCCAGAACAGTA	660
Qy	673	ATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCTGAACAATTAATA	732
Db	661	ATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCTGAACAATTAATA	720
Qy	733	CTCTGTGTTTTAGAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGATGTGATGAATAC	792

Db	721	CTCTGTGTTTTAGAAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGATGTGATGAATAC	780
Qy	793	TTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGTATAATGCTTGGG	852
Db	781	TTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGTATAATGCTTGGG	840
Qy	853	AGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAACTGCCAATGGAC	912
Db	841	AGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAACTGCCAATGGAC	900
Qy	913	TGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCATATATGAATGGA	972
Db	901	TGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCATATATGAATGGA	960
Qy	973	GAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATAAAAAATCTTTGT	1032
Db	961	GAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATAAAAAATCTTTGT	1020
Qy	1033	GCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTTCGAACAGGTATC	1092
Db	1021	GCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTTCGAACAGGTATC	1080
Qy	1093	TACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTACCTTGTTCCAAT	1152
Db	1081	TACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTACCTTGTTCCAAT	1140
Qy	1153	CCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCTCGTATCTTCTCGTGTGCT	1212
Db	1141	CCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCTCGTATCTTCTCGTGTGCT	1200
Qy	1213	CGACTTTGCCTTTCCATTGTCTCTGTTAAAGGCCGAAAGGGTGCTAAAGAGGAACACTGT	1272
Db	1201	CGACTTTGCCTTTCCATTGTCTCTGTTAAAGGCCGAAAGGGTGCTAAAGAGGAACACTGT	1260
Qy	1273	CCATTGGCATGGGGAATATAAACTTGTTTGATTACACAGACACTCTAGTATCTGGAAAA	1332
Db	1261	CCATTGGCATGGGGAATATAAACTTGTTTGATTACACAGACACTCTAGTATCTGGAAAA	1320
Qy	1333	ATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTGCTGAACCTATTGGT	1392
Db	1321	ATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTGCTGAACCTATTGGT	1380
Qy	1393	GTTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAGTTTGACTGGTTC	1452
Db	1381	GTTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAGTTTGACTGGTTC	1440
Qy	1453	AGCAGTGTGGTAAAGTTCCAGATATGTGAGTGAAGAGCATGCCAATTGGTCTGTA	1512

Db	1441	AGCAGTGTGGTAAAGTTCCCGAGATATGTCTAGTGATTGAAGAGCATGCCAATTGGTCTGTA	1500
Qy	1513	TCCCAGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGACTAGCTAGAGAC	1572
Db	1501	TCCCAGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGACTAGCTAGAGAC	1560
Qy	1573	AATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACACGAGATCCTCTC	1632
Db	1561	AATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACACGAGATCCTCTC	1620
Qy	1633	TCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGTGTAAC	1692
Db	1621	TCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGTGTAAC	1680
Qy	1693	ATCCCCGAAATTTCTACCAAATTGCTTCTGTCTGTTAAATGGAATTTAGAGATGAAGTA	1752
Db	1681	ATCCCCGAAATTTCTACCAAATTGCTTCTGTCTGTTAAATGGAATTTAGAGATGAAGTA	1740
Qy	1753	GCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCTATGGAA	1812
Db	1741	GCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCTATGGAA	1800
Qy	1813	CTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTTCCGGTGCTTGGAA	1872
Db	1801	CTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTTCCGGTGCTTGGAA	1860
Qy	1873	AAATATTTAACAGATGACAAACTTTTCTCAGTATTTAATTCAGCTAGTACAGGTCCTAAAA	1932
Db	1861	AAATATTTAACAGATGACAAACTTTTCTCAGTATTTAATTCAGCTAGTACAGGTCCTAAAA	1920
Qy	1933	TATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAAGCATTGACTAAT	1992
Db	1921	TATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAAGCATTGACTAAT	1980
Qy	1993	CAAAGGATTGGGCACTTTTTCTTTTGGCATTAAAACTGAGATGCACAATAAAACAGTT	2052
Db	1981	CAAAGGATTGGGCACTTTTTCTTTTGGCATTAAAACTGAGATGCACAATAAAACAGTT	2040
Qy	2053	AGCCAGAGGTTTTGGCCTGCTTTTGGAGTCCATTGTCTGTCATGTGGGATGTATTTGAAG	2112
Db	2041	AGCCAGAGGTTTTGGCCTGCTTTTGGAGTCCATTGTCTGTCATGTGGGATGTATTTGAAG	2100
Qy	2113	CACCTGAATAGGCAAGTCGAGGCAATGGAAGAGCTCATTAACCTAACTGACATTCTCAA	2172
Db	2101	CACCTGAATAGGCAAGTCGAGGCAATGGAAGAGCTCATTAACCTAACTGACATTCTCAA	2160
Qy	2173	CAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTAGTTGAGCAAATGAGG	2232
Db	2161	CAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTAGTTGAGCAAATGAGG	2220

Qy	2233	CGACCAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAACCTGCTCATCAA	2292
Db	2221	CGACCAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAACCTGCTCATCAA	2280
Qy	2293	CTAGGAAACCTCAGGCTTAAAGAGTGTGCAATTATGTCTTCTGCAAAAAGGCCACTGTGG	2352
Db	2281	CTAGGAAACCTCAGGCTTAAAGAGTGTGCAATTATGTCTTCTGCAAAAAGGCCACTGTGG	2340
Qy	2353	TTGAATTGGGAGAAGCCAGACATCATGTGAGAGTTACTGTTTCAGAACAAATGAGATCATC	2412
Db	2341	TTGAATTGGGAGAAGCCAGACATCATGTGAGAGTTACTGTTTCAGAACAAATGAGATCATC	2400
Qy	2413	TTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATTATTCGTATTATG	2472
Db	2401	TTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATTATTCGTATTATG	2460
Qy	2473	GAAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTATGGTTGTCTGTCA	2532
Db	2461	GAAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTATGGTTGTCTGTCA	2520
Qy	2533	ATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCAGAAATTTCTCACACTATTATGCAAAAT	2592
Db	2521	ATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCAGAAATTTCTCACACTATTATGCAAAAT	2580
Qy	2593	CAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACACTACATCAGTGG	2652
Db	2581	CAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACACTACATCAGTGG	2640
Qy	2653	CTCAAAGACAAGAACAAGGAGAAATATATGATGCAGCCATTGACCTGTTTACACGTTCA	2712
Db	2641	CTCAAAGACAAGAACAAGGAGAAATATATGATGCAGCCATTGACCTGTTTACACGTTCA	2700
Qy	2713	TGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGTCACAATAGTAAC	2772
Db	2701	TGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGTCACAATAGTAAC	2760
Qy	2773	ATCATGGTGAAAGACGATGGACAACGTGTTTCATATAGATTTTGGACACTTTTGGATCAC	2832
Db	2761	ATCATGGTGAAAGACGATGGACAACGTGTTTCATATAGATTTTGGACACTTTTGGATCAC	2820
Qy	2833	AAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTGTTTTGACACAGGATTTT	2892
Db	2821	AAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTGTTTTGACACAGGATTTT	2880
Qy	2893	TTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAATTTGAGAGGTTT	2952
Db	2881	TTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAATTTGAGAGGTTT	2940

Qy	2953	CAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAATCTCTTCATAAAAT	3012
Db	2941		3000
Qy	3013	CTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTTGATGACATTGCA	3072
Db	3001		3060
Qy	3073	TACATTGCAAGACCCCTAGCCTTAGATAAACTGAGCAAGAGGCTTTGGAGTATTTTCATG	3132
Db	3061		3120
Qy	3133	AAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAATGGATTGGATCTTCCAC	3192
Db	3121		3180
Qy	3193	ACAATTAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAAGCTCACTCTGGA	3252
Db	3181		3240
Qy	3253	TTCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCATAGGAATTGCAC	3312
Db	3241		3300
Qy	3313	AATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACTATATAATTTAAA	3372
Db	3301		3360
Qy	3373	TAATGTAACGCAACAGGGTTTGATAGCACTTAACTAGTTTCATTTCAAAA	3424
Db	3361		3412

RESULT 10

ADU05935

ID ADU05935 standard; DNA; 3423 BP.

XX

AC ADU05935;

XX

DT 27-JAN-2005 (first entry)

XX

DE Novel bronchial cancer-associated human gene SeqID157.

XX

KW bronchial cancer; cytostatic; tumour-associated protein;

KW cancer detection; metastasis; tumour; gene; ds; human.

XX

OS Homo sapiens.

XX

PN DE10316701-A1.


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|||||
Db      61  CCCCCAAGAACTCTAGTGGAAATGTTTACTACCAATGGAATGATAGTGACTTTAGAATGC 120

Qy      121  CTCCGTGAGGCTACATTAGTAACATAAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC 180
|||||
Db      121  CTCCGTGAGGCTACATTAGTAACATAAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC 180

Qy      181  CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA 240
|||||
Db      181  CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA 240

Qy      241  GCAGAAAGGGAAGAATTTTTTATGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTCAA 300
|||||
Db      241  GCAGAAAGGGAAGAATTTTTTATGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTCAA 300

Qy      301  CCATTTTTTAAAGTAATTGAACCAAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA 360
|||||
Db      301  CCATTTTTTAAAGTAATTGAACCAAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA 360

Qy      361  ATTTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA 420
|||||
Db      361  ATTTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA 420

Qy      421  CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAGAAAGCTGTGGATCTTAGGGATCTT 480
|||||
Db      421  CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAGAAAGCTGTGGATCTTAGGGATCTT 480

Qy      481  AATTACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG 540
|||||
Db      481  AATTACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG 540

Qy      541  CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTGGGTA 600
|||||
Db      541  CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTGGGTA 600

Qy      601  ATAGTTTCTCCAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG 660
|||||
Db      601  ATAGTTTCTCCAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG 660

Qy      661  CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT 720
|||||
Db      661  CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT 720

Qy      721  GAACAATTAAGTCTGTGTTTTAGAAATATCAGGGCAAGTACATTTTAAAGTGTGTGGA 780
|||||
Db      721  GAACAATTAAGTCTGTGTTTTAGAAATATCAGGGCAAGTACATTTTAAAGTGTGTGGA 780

Qy      781  TGTGATGAATACTTCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT 840
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Db	781	TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Qy	841	ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Db	841	ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Qy	901	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	960
Db	901	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	960
Qy	961	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA	1020
Db	961	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA	1020
Qy	1021	AAAATTCCTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT	1080
Db	1021	AAAATTCCTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT	1080
Qy	1081	CGAACAGGTATCTACCATGGAGGAGAACCCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Db	1081	CGAACAGGTATCTACCATGGAGGAGAACCCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Qy	1141	CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCTGATCTT	1200
Db	1141	CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCTGATCTT	1200
Qy	1201	CCTCGTGTGCTCGACTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA	1260
Db	1201	CCTCGTGTGCTCGACTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA	1260
Qy	1261	GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA	1320
Db	1261	GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA	1320
Qy	1321	GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1380
Db	1321	GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1380
Qy	1381	AACCCATTGGTGTTACTGGATCAAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAG	1440
Db	1381	AACCCATTGGTGTTACTGGATCAAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAG	1440
Qy	1441	TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Db	1441	TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Qy	1501	AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Db	1501	AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560

Qy	1561	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620
Db	1561	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620
Qy	1621	CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAAGATTTTCTATGGAGTCACAGACAC	1680
Db	1621	CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAAGATTTTCTATGGAGTCACAGACAC	1680
Qy	1681	TATTGTGTAACATATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT	1740
Db	1681	TATTGTGTAACATATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT	1740
Qy	1741	AGAGATGAAGTAGCCAGATGTATTGCTTGGTAAAAGATTGGCTCCAATCAAACCTGAA	1800
Db	1741	AGAGATGAAGTAGCCAGATGTATTGCTTGGTAAAAGATTGGCTCCAATCAAACCTGAA	1800
Qy	1801	CAGGCTATGGAACCTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT	1860
Db	1801	CAGGCTATGGAACCTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT	1860
Qy	1861	CGGTGCTTGGAAAAATATTTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA	1920
Db	1861	CGGTGCTTGGAAAAATATTTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA	1920
Qy	1921	CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTACTGAAGAAA	1980
Db	1921	CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTACTGAAGAAA	1980
Qy	1981	GCATTGACTAATCAAAGGATTGGGCACTTTTCTTTTGGCATTAAATCTGAGATGCAC	2040
Db	1981	GCATTGACTAATCAAAGGATTGGGCACTTTTCTTTTGGCATTAAATCTGAGATGCAC	2040
Qy	2041	AATAAAACAGTTAGCCAGAGGTTGGCCTGCTTTTGGAGTCCTATTGTCGTCATGTGGG	2100
Db	2041	AATAAAACAGTTAGCCAGAGGTTGGCCTGCTTTTGGAGTCCTATTGTCGTCATGTGGG	2100
Qy	2101	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTAACT	2160
Db	2101	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTAACT	2160
Qy	2161	GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTAGTT	2220
Db	2161	GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTAGTT	2220
Qy	2221	GAGCAAATGAGGCGACCAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC	2280
Db	2221	GAGCAAATGAGGCGACCAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC	2280

Qy	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTGCAATTATGTCTTCTGCAAAA	2340
Db	2281		2340
Qy	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTGAGAGTTACTGTTTCAGAAC	2400
Db	2341		2400
Qy	2401	AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT	2460
Db	2401		2460
Qy	2461	ATTGCTATTATGGAATAATCTGGCAAAATCAAGGCTTGTATCTTCGAATGTTACCTTAT	2520
Db	2461		2520
Qy	2521	GGTTGCTGTCAATCGGTGACTGTGTGGACTTATTGAGGTGGTGCAGAAATTCACACT	2580
Db	2521		2580
Qy	2581	ATTATGCAAAATTCAGTGCAAAGCGGCTTGAAGGTGCACTGCAGTTCAACAGCCACACA	2640
Db	2581		2640
Qy	2641	CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG	2700
Db	2641		2700
Qy	2701	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760
Db	2701		2760
Qy	2761	CACAATAGTAACATCATGGTGAAAGACGATGGACAACCTGTTTCATATAGATTTTGGACAC	2820
Db	2761		2820
Qy	2821	TTTTTGGATCACAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG	2880
Db	2821		2880
Qy	2881	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940
Db	2881		2940
Qy	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT	3000
Db	2941		3000
Qy	3001	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060

Db	3001	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060
Qy	3061	GATGACATTGCATACATTTCGAAAGACCCCTAGCCTTAGATAAACTGAGCAAGAGGCTTTG	3120
Db	3061	GATGACATTGCATACATTTCGAAAGACCCCTAGCCTTAGATAAACTGAGCAAGAGGCTTTG	3120
Qy	3121	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Db	3121	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Qy	3181	TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAAATGAAA	3240
Db	3181	TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAAATGAAA	3240
Qy	3241	GCTCACTCTGGATTCCCACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA	3300
Db	3241	GCTCACTCTGGATTCCCACTGCACTG-TAATAACTCTCAGCAGGCAAAGACCGATTGCA	3299
Qy	3301	TAGGAATTGCACAATCCATGAACAGCATTAGATTACAGCAAGAACAGAAATAAAATACT	3360
Db	3300	TAGGAATTGCACAATCCATGAACAGCATTAGATTACAGCAAGAACAGAAATAAAATACT	3359
Qy	3361	ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAACTAGTTCATTTT	3420
Db	3360	ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAACTAGTTCATTTT	3419
Qy	3421	AAAA 3424	
Db	3420	AAAA 3423	

RESULT 11

ARC02473

ID ARC02473 standard; DNA; 3426 BP.

XX

AC ARC02473;

XX

DT 10-JUL-2008 (first entry)

XX

DE DNA fragments of a human Tox gene, 46524.

XX

KW DNA microarray; gene expression; drug screening; ds; Tox.

XX

OS Homo sapiens.

XX

PN US2007072175-A1.

XX

PD 29-MAR-2007.

XX
PF 15-MAY-2006; 2006US-00433832.
XX
PR 13-MAY-2005; 2005US-0680473P.
PR 13-MAY-2005; 2005US-0680544P.
XX
PA (BIOJ) BIOGEN IDEC MA INC.
XX
PI Cooper MT, Kinch D, Rosenberg M, Subramaniam SS, Szak ST, Li H;
PI Bandaru R, Derbel M;
XX
DR WPI; 2007-432796/41.
XX
PT New nucleotide array comprises polynucleotide probes complementary to, or
PT fragments of, Cynomolgus monkey genes, useful for detecting changes in
PT gene expression upon administration of a therapeutic agent.
XX
PS Claim 18; SEQ ID NO 46524; 33pp; English.
XX
CC The new invention relates to a nucleotide array for detecting changes in
CC gene expression upon administration of a therapeutic agent. The
CC microarray has polynucleotide probes complementary to, or fragments of,
CC Cynomolgus monkey genes, where each polynucleotide probe is immobilized
CC to a discrete and known spot on a solid support. The polynucleotide
CC probes are complementary to, or fragments of, any portion of an ortholog
CC of a human gene, preferably a Tox gene. The probes are any of SEQ ID NO.
CC 8882-9186. The probes are also complementary to, or fragments of, any
CC portion of any of SEQ ID NO. 1-8881 or 9187-18598. The nucleotide array
CC has at least one probe complementary to, or a fragment of, any portion of
CC any human gene, where the probe from a human gene is any of SEQ ID NO.
CC 43226-48714, or is complementary to, or a fragment of, any portion of any
CC of SEQ ID NO. 43450-48714. The array has at least one probe complementary
CC to, or a fragment of, any portion of any Rhesus monkey gene, where the
CC probe from a Rhesus monkey gene is any of SEQ ID NO. 35841-36074, or is
CC complementary to, or a fragment of, any portion of any of SEQ ID NO.
CC 18599-35840 or 36075-43225. It also has at least one probe complementary
CC to, or a fragment of, any portion of a Rhesus monkey gene and at least
CC one probe complementary to, or a fragment of, any portion of any human
CC gene. The nucleotide array is useful for detecting changes in gene
CC expression upon administration of a therapeutic agent. It can be used for
CC characterizing the actions, targets, and toxicities of therapeutic agents
CC in primates, e.g. a human, a Cynomolgus monkey, or a Rhesus monkey. This
CC sequence is a DNA fragment of a human Tox gene.
XX
SQ Sequence 3426 BP; 1138 A; 623 C; 703 G; 962 T; 0 U; 0 Other;

Query Match 97.5%; Score 3339.6; DB 6; Length 3426;
Best Local Similarity 98.8%;
Matches 3385; Conservative 0; Mismatches 39; Indels 2; Gaps 2;

Qy	1	AGGATCAGAACAAATGCCTCCAAGACCATCATCAGGTGAAGTGTGGGGCATCCACTTGATG	60
Db	1	AGAATCAGAACAAATGCCTCCACGACCATCATCAGGTGAAGTGTGGGGCATCCACTTGATG	60
Qy	61	CCCCCAAGAAATCCTAGTGAATGTTTACTACCAATGGAATGATAGTGACTTTAGAATGC	120
Db	61	CCCCCAAGAAATCCTAGTAGAATGTTTACTACCAATGGAATGATAGTGACTTTAGAATGC	120
Qy	121	CTCCGTGAGGCTACATTAGTAACATAAAGCATGAAGTATTTAAAGAAGCAAGAAAATAC	180
Db	121	CTCCGTGAGGCTACATTAATAACCATAAAGCATGAAGTATTTAAAGAAGCAAGAAAATAC	180
Qy	181	CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA	240
Db	181	CCCCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACTCAAGAA	240
Qy	241	GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAA	300
Db	241	GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGACCTTCGGCTTTTTCAA	300
Qy	301	CCATTTTTTAAAGTAATTGAACCAAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Db	301	CCCTTTTTTAAAGTAATTGAACCAAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Qy	361	ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA	420
Db	361	ATTGGTTTTGCTATCGGCATGCCAGTGTGTGAATTTGATATGGTTAAAGATCCAGAAGTA	420
Qy	421	CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAGAAGCTGTGGATCTTAGGGATCTT	480
Db	421	CAGGACTTCCGAAGAAATATTCTGAACGTTTGTAAGAAGCTGTGGATCTTAGGGACCTC	480
Qy	481	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTACCAGAG	540
Db	481	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCTCCAAATGTAGAATCTTACCAGAA	540
Qy	541	CTGCCAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTGGGTA	600
Db	541	TTGCCAAGCACATATATAATAAATTAGATAAAGGGCAAATAATAGTGGTGATCTGGGTA	600
Qy	601	ATAGTTTCTCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG	660
Db	601	ATAGTTTCTCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTA	660
Qy	661	CCAGAACAAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT	720
Db	661	CCAGAACAAAGTAATTGCTGAAGCAATCAGGAAAAAACTCGAAGTATGTTGCTATCCTCT	720

Qy	721	GAACAATTAATACTCTGTGTTTTAGAAATATCAGGGCAAGTACATTTTAAAGTGTGTGGA	780
Db	721	GAACAATAATACTCTGTGTTTTAGAAATATCAGGGCAAGTATATTTTAAAGTGTGTGGA	780
Qy	781	TGTGATGAATACTTCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Db	781	TGTGATGAATACTTCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Qy	841	ATAATGCTTGGGAGGATGCCCAATTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Db	841	ATAATGCTTGGGAGGATGCCCAATTGATGTTGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Qy	901	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	960
Db	901	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	960
Qy	961	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA	1020
Db	961	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGTGCCTCAGAATA	1020
Qy	1021	AAAATTCCTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT	1080
Db	1021	AAAATTCCTTGTGCAACCTACGTGAATGTAAATATTCGAGACATTGATAAGATCTATGTT	1080
Qy	1081	CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Db	1081	CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Qy	1141	CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCTGATCTT	1200
Db	1141	CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCTGATCTT	1200
Qy	1201	CCTCGTGTGCTCGACTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA	1260
Db	1201	CCTCGTGTGCTCGACTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA	1260
Qy	1261	GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACAGACACTCTA	1320
Db	1261	GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACAGACACTCTA	1320
Qy	1321	GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTGCTG	1380
Db	1321	GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTGCTG	1380
Qy	1381	AACCTATTGGTGTTACTGGATCAAATCCAAATAAGAACTCCATGCTTAGAGTTGGAG	1440
Db	1381	AACCTATTGGTGTTACTGGATCAAATCCAAATAAGAACTCCATGCTTAGAGTTGGAG	1440
Qy	1441	TTTGAAGTTCAGCAGTGTGGTAAAGTTCCAGATATGTCAGTGATTGAAGAGCATGCC	1500

Db	1441	TTTGACTGGTTTCAGCAGTGTGGTAAAGTTCACAGATATGTCAGTGATTGAAGAGCATGCC	1500	
Qy	1501	AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCACGCAGGACTGAGTAACAGA	1560	
Db	1501	AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCACGCAGGACTGAGTAACAGA	1560	
Qy	1561	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620	
Db	1561	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620	
Qy	1621	CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAAGATTTTCTATGGAGTCACAGACAC	1680	
Db	1621	CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAAGATTTTCTATGGAGTCACAGACAC	1680	
Qy	1681	TATTGTGTAACATATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT	1740	
Db	1681	TATTGTGTAACATATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT	1740	
Qy	1741	AGAGATGAAGTAGCCAGATGTATTGCTTGGTAAAAGATTGGCTCCAATCAAACCTGAA	1800	
Db	1741	AGAGATGAAGTAGCCAGATGTATTGCTTGGTAAAAGATTGGCTCCAATCAAACCTGAA	1800	
Qy	1801	CAGGCTATGGAACCTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT	1860	
Db	1801	CAGGCTATGGAACCTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT	1860	
Qy	1861	CGGTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA	1920	
Db	1861	CGGTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA	1920	
Qy	1921	CAGGTCCTAAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTACTGAAGAAA	1980	
Db	1921	CAGGTCCTAAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTACTGAAGAAA	1980	
Qy	1981	GCATTGACTAATCAAAGGATTGGGCACCTTTTCTTTTGGCATTAAAAATCTGAGATGCAC	2040	
Db	1981	GCATTGACTAATCAAAGGATTGGGCACCTTTTCTTTTGGCATTAAAAATCTGAGATGCAC	2040	
Qy	2041	AATAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2100	
Db	2041	AATAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2100	
Qy	2101	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACTTAACT	2160	
Db	2101	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACTTAACT	2160	
Qy	2161	GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTAGTGT	2220	

Db	2161	GACATTCTCAAACAGGAGAAGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT	2220
Qy	2221	GAGCAAATGAGGCGACCAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC	2280
Db	2221	GAGCAAATGAGGCGACCAGATTTTCATGGATGCTCTACAGGGCTTTCTGTCTCCTCTAAAC	2280
Qy	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTGCAATTATGTCTTCTGCAAAA	2340
Db	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTGAAGAGTGTGCAATTATGTCTTCTGCAAAA	2340
Qy	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC	2400
Db	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC	2400
Qy	2401	AATGAGATCATCTTTAAAAATGGGGATGATTACGGCAAGATATGCTAACACTTCAAATT	2460
Db	2401	AATGAGATCATCTTTAAAAATGGGGATGATTACGGCAAGATATGCTAACACTTCAAATT	2460
Qy	2461	ATTCTGATTATGAAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT	2520
Db	2461	ATTCTGATTATGAAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT	2520
Qy	2521	GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCACACT	2580
Db	2521	GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCACACT	2580
Qy	2581	ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2640
Db	2581	ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2640
Qy	2641	CTACATCAGTGGCTCAAAGACAAGAACAAGGAGAAATATATGATGCAGCCATTGACCTG	2700
Db	2641	CTACATCAGTGGCTCAAAGACAAGAACAAGGAGAAATATATGATGCAGCCATTGACCTG	2700
Qy	2701	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760
Db	2701	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760
Qy	2761	CACAATAGTAACATCATGGTGAAAGACGATGGACAACCTGTTTCATATAGATTTTGGACAC	2820
Db	2761	CACAATAGTAACATCATGGTGAAAGACGATGGACAACCTGTTTCATATAGATTTTGGACAC	2820
Qy	2821	TTTTTGGATCACAGAAGAAAAAATTGGTTATAAACGAGAAGCTGTGCCATTGTGTTTG	2880
Db	2821	TTTTTGGATCACAGAAGAAAAAATTGGTTATAAACGAGAAGCTGTGCCATTGTGTTTG	2880
Qy	2881	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940
Db	2881	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940

Qy	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT	3000
Db	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT	3000
Qy	3001	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060
Db	3001	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060
Qy	3061	GATGACATTGCATACATTGAAAAGACCCTAGCCTTAGATAAACTGAGCAAGAGGCTTTG	3120
Db	3061	GATGACATTGCATACATTGAAAAGACCCTAGCCTTAGATAAACTGAGCAAGAGGCTTTG	3120
Qy	3121	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Db	3121	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Qy	3181	TGGATCTTCCACACAATTAACAGCATGCATTGAACTG-AAAGATAACTGAGAAAAATGAA	3239
Db	3181	TGGATCTTCCACACAATTAACAGCATGCATTGAACTGAAAAGATAACTGAGAAAAATGAA	3240
Qy	3240	AGCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGC	3299
Db	3241	AGCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGC	3300
Qy	3300	ATAGGAATTGCACAATCCATGAACAGCATTAG-ATTTACAGCAAGAACAGAAATAAAATA	3358
Db	3301	ATAGGAATTGCACAATCCATGAACAGCATTAGAAATTTACAGCAAGAACAGAAATAAAATA	3360
Qy	3359	CTATATAATTTAAATAATGTAAACGCAACAGGGTTTGATAGCACTTAACTAGTTCATT	3418
Db	3361	CTATATAATTTAAATAATGTAAACGCAACAGGGTTTGATAGCACTTAACTAGTTCATT	3420
Qy	3419	TCAAAA	3424
Db	3421	TCAAAA	3426

RESULT 12

AEK54940

ID AEK54940 standard; DNA; 3724 BP.

XX

AC AEK54940;

XX

DT 11-JUN-2007 (revised)

DT 16-NOV-2006 (first entry)

XX

DE Human PIK3CA DNA, SEQ ID NO:7.

XX

KW phosphoinositide-3-kinase, catalytic, alpha; PIK3CA; genetic marker;
 KW screening; adenocarcinoma; neoplasm; cytostatic; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO2006094149-A2.
 XX
 PD 08-SEP-2006.
 XX
 PF 01-MAR-2006; 2006WO-US007493.
 XX
 PR 01-MAR-2005; 2005US-0657841P.
 XX
 PA (EXAC-) EXACT SCI CORP.
 XX
 PI Shuber AP;
 XX
 DR WPI; 2006-680485/70.
 DR REFSEQ; NM_006218.
 DR PC:NCBI; gi54792081.
 DR PC_ENCPRO:NCBI; gi54792082.
 XX
 PT Screening for adenoma in a subject, comprises testing a sample for the
 PT presence of each of a panel of genetic markers, where the panel is more
 PT than 60% informative for adenoma.
 XX
 PS Disclosure; SEQ ID NO 7; 79pp; English.
 XX
 CC The invention relates to a method for screening a subject for the
 CC presence of adenoma. The method comprises interrogating a sample from the
 CC subject for each of a panel of genetic markers, where the panel is more
 CC than 60% informative for adenoma, and where the presence of one or more
 CC of the markers is indicative of adenoma. Also described are: (1) a method
 CC of detecting indicia of adenoma, by assaying a sample from a subject for
 CC the presence of one or more genetic abnormalities from a group of genetic
 CC abnormalities that is more than 60% informative for adenoma; (2) a method
 CC of detecting adenoma in a subject, by performing an assay on a sample
 CC from the subject that is more than 60% informative for adenoma; and (3) a
 CC kit comprising a group of oligonucleotides, where each oligonucleotide is
 CC adapted for interrogating a genetic locus for the presence of a marker
 CC from a panel that is at least 60% informative for adenoma. The methods
 CC and kit of the invention are useful for screening for adenoma in a
 CC subject. The adenoma is especially a colonic and/or invasive adenoma. The
 CC methods can detect adenoma at an early stage with a high level of
 CC confidence, increasing the chances of successful treatment. This sequence
 CC represents a human DNA sequence that can be used as a genetic marker in
 CC the method of the invention.
 CC
 CC Revised record issued on 11-JUN-2007 : Enhanced with precomputed

CC information from BOND.

XX

SQ Sequence 3724 BP; 1242 A; 684 C; 763 G; 1035 T; 0 U; 0 Other;

Query Match 97.5%; Score 3339.6; DB 4; Length 3724;
 Best Local Similarity 98.8%;
 Matches 3385; Conservative 0; Mismatches 39; Indels 2; Gaps 2;

Qy	1	AGGATCAGAACATGCCTCCAGACCATCATCAGGTGAAGTGTGGGGCATCCACTTGATG	60
Db	146	AGAATCAGAACATGCCTCCAGACCATCATCAGGTGAAGTGTGGGGCATCCACTTGATG	205
Qy	61	CCCCAAGAATCCTAGTGAATGTTTACTACCAATGGAATGATAGTGACTTTAGAATGC	120
Db	206	CCCCAAGAATCCTAGTGAATGTTTACTACCAATGGAATGATAGTGACTTTAGAATGC	265
Qy	121	CTCGTGAGGCTACATTAGTAACATATAAAGCATGAAGTATTTAAAGAAGCAAGAAAATAC	180
Db	266	CTCGTGAGGCTACATTAGTAACATATAAAGCATGAAGTATTTAAAGAAGCAAGAAAATAC	325
Qy	181	CCTCTCCATCAACTTCTCAAGATGAATCTTCTTACATTTTCGTAAGTGTACCCAAGAA	240
Db	326	CCCCTCCATCAACTTCTCAAGATGAATCTTCTTACATTTTCGTAAGTGTACTCAAGAA	385
Qy	241	GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTCAA	300
Db	386	GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGACCTTCGGCTTTTCAA	445
Qy	301	CCATTTTTTAAAGTAATTGAACCAAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Db	446	CCCTTTTTTAAAGTAATTGAACCAAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	505
Qy	361	ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA	420
Db	506	ATTGGTTTTGCTATCGGCATGCCAGTGTGGAATTTGATATGGTTAAAGATCCAGAAGTA	565
Qy	421	CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAGAAGCTGTGGATCTTAGGGATCTT	480
Db	566	CAGGACTTCCGAAGAAATATTCTGAACGTTTGTAAGAAGCTGTGGATCTTAGGGACCTC	625
Qy	481	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG	540
Db	626	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCTCCAAATGTAGAATCTTCACCAGAA	685
Qy	541	CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTA	600
Db	686	TTGCCAAAGCACATATATAATAAATTAGATAAAGGGCAAATAATAGTGGTGATCTGGGTA	745
Qy	601	ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAATCAACCATGACTGTGTG	660

Db	746		ATAGTTTCTCCAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTA	805
Qy	661		CCAGAACAAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAAGTATGTTGCTATCATCT	720
Db	806		CCAGAACAAAGTAATTGCTGAAGCAATCAGGAAAAAACTCGAAGTATGTTGCTATCTCT	865
Qy	721		GAACAATTAAGTCTGTGTTTGTAGAAATATCAGGGCAAGTACATTTTAAAGTGTGTGGA	780
Db	866		GAACAATTAAGTCTGTGTTTGTAGAAATATCAGGGCAAGTATTTTAAAGTGTGTGGA	925
Qy	781		TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Db	926		TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	985
Qy	841		ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Db	986		ATAATGCTTGGGAGGATGCCCAATTTGATGTTGATGGCTAAAGAAAGCCTTTATTCTCAA	1045
Qy	901		CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	960
Db	1046		CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	1105
Qy	961		TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA	1020
Db	1106		TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGTGCACCTCAGAATA	1165
Qy	1021		AAAATCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT	1080
Db	1166		AAAATCTTTGTGCAACCTACGTGAATGTAAATATTCGAGACATTGATAAGATCTATGTT	1225
Qy	1081		CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAAATGTGAACACTCAAAGAGTA	1140
Db	1226		CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAAATGTGAACACTCAAAGAGTA	1285
Qy	1141		CCTTGTTCCAATCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCTGATCTT	1200
Db	1286		CCTTGTTCCAATCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCTGATCTT	1345
Qy	1201		CCTCGTGTGCTCGACTTTGCCTTTCCATTTGCTCTGTAAAGGCCGAAAGGGTGCTAAA	1260
Db	1346		CCTCGTGTGCTCGACTTTGCCTTTCCATTTGCTCTGTAAAGGCCGAAAGGGTGCTAAA	1405
Qy	1261		GAGGAACACTGTCCATTGGCATGGGGAATATAAACTTGTGTTGATTACACAGACACTCTA	1320
Db	1406		GAGGAACACTGTCCATTGGCATGGGGAATATAAACTTGTGTTGATTACACAGACACTCTA	1465
Qy	1321		GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1380

Db	1466	GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1525
Qy	1381	AACCTATTGGTGTACTGGATCAAATCCAAATAAGAACTCCATGCTTAGAGTTGGAG	1440
Db	1526	AACCTATTGGTGTACTGGATCAAATCCAAATAAGAACTCCATGCTTAGAGTTGGAG	1585
Qy	1441	TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Db	1586	TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCAGATATGTCAGTGATTGAAGAGCATGCC	1645
Qy	1501	AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Db	1646	AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1705
Qy	1561	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620
Db	1706	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1765
Qy	1621	CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAAGATTTTCTATGGAGTCACAGACAC	1680
Db	1766	CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAAGATTTTCTATGGAGTCACAGACAC	1825
Qy	1681	TATTGTGTAACATATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT	1740
Db	1826	TATTGTGTAACATATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT	1885
Qy	1741	AGAGATGAAGTAGCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1800
Db	1886	AGAGATGAAGTAGCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1945
Qy	1801	CAGGCTATGGAACCTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTGTCTGTT	1860
Db	1946	CAGGCTATGGAACCTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTGTCTGTT	2005
Qy	1861	CGGTGCTTGGA AAAATATTTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA	1920
Db	2006	CGGTGCTTGGA AAAATATTTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA	2065
Qy	1921	CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTACTGAAGAAA	1980
Db	2066	CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTACTGAAGAAA	2125
Qy	1981	GCATTGACTAATCAAAGGATTGGGCACCTTTTCTTTTGGCATTAAATCTGAGATGCAC	2040
Db	2126	GCATTGACTAATCAAAGGATTGGGCACCTTTTCTTTTGGCATTAAATCTGAGATGCAC	2185
Qy	2041	AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2100
Db	2186	AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2245

Qy	2101	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTAACT	2160
Db	2246	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTAACT	2305
Qy	2161	GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTAGTT	2220
Db	2306	GACATTCTCAAACAGGAGAGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTAGTT	2365
Qy	2221	GAGCAAAATGAGGCGACCAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC	2280
Db	2366	GAGCAAAATGAGGCGACCAGATTTTCATGGATGCTCTACAGGGCTTTCTGTCTCCTCTAAAC	2425
Qy	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTGCAATTATGTCTTCTGCAAAA	2340
Db	2426	CCTGCTCATCAACTAGGAAACCTCAGGCTTGAAGAGTGTGCAATTATGTCTTCTGCAAAA	2485
Qy	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTGAGATTACTGTTTCAGAAC	2400
Db	2486	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTGAGATTACTGTTTCAGAAC	2545
Qy	2401	AATGAGATCATCTTTAAAAATGGGGATGATTACGGCAAGATATGCTAACACTTCAAATT	2460
Db	2546	AATGAGATCATCTTTAAAAATGGGGATGATTACGGCAAGATATGCTAACACTTCAAATT	2605
Qy	2461	ATTCGTATTATGAAAAATATCTGGCAAAATCAAGGCTTGATCTTCGAATGTTACCTTAT	2520
Db	2606	ATTCGTATTATGAAAAATATCTGGCAAAATCAAGGCTTGATCTTCGAATGTTACCTTAT	2665
Qy	2521	GGTTGCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCAGACT	2580
Db	2666	GGTTGCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCAGACT	2725
Qy	2581	ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2640
Db	2726	ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2785
Qy	2641	CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG	2700
Db	2786	CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG	2845
Qy	2701	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760
Db	2846	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2905
Qy	2761	CACAATAGTAACATCATGGTGAAAGACGATGGACAACTGTTTCATATAGATTTTGGACAC	2820
Db	2906	CACAATAGTAACATCATGGTGAAAGACGATGGACAACTGTTTCATATAGATTTTGGACAC	2965

Qy	2821	TTTTTGGATCACAGAAGAAAAAATTGGTTATAAACGAGACGTGTGCCATTGTGTTTG	2880
Db	2966	TTTTTGGATCACAGAAGAAAAAATTGGTTATAAACGAGACGTGTGCCATTGTGTTTG	3025
Qy	2881	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940
Db	3026	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	3085
Qy	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT	3000
Db	3086	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT	3145
Qy	3001	CTCTTCATAAATCTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060
Db	3146	CTCTTCATAAATCTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3205
Qy	3061	GATGACATTGCATACATTGAAAAGACCCTAGCCTTAGATAAACTGAGCAAGAGGCTTTG	3120
Db	3206	GATGACATTGCATACATTGAAAAGACCCTAGCCTTAGATAAACTGAGCAAGAGGCTTTG	3265
Qy	3121	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Db	3266	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3325
Qy	3181	TGGATCTTCCACACAATTAAACAGCATGCATTGAACTG-AAAGATAACTGAGAAAAATGAA	3239
Db	3326	TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAAGATAACTGAGAAAAATGAA	3385
Qy	3240	AGCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGC	3299
Db	3386	AGCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGC	3445
Qy	3300	ATAGGAATTGCACAATCCATGAACAGCATTAG-ATTACAGCAAGAACAGAAATAAAATA	3358
Db	3446	ATAGGAATTGCACAATCCATGAACAGCATTAGATTACAGCAAGAACAGAAATAAAATA	3505
Qy	3359	CTATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAACTAGTTCATT	3418
Db	3506	CTATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAACTAGTTCATT	3565
Qy	3419	TCAAAA 3424	
Db	3566	TCAAAA 3571	

RESULT 13

AER29796

ID AER29796 standard; DNA; 3724 BP.

XX

AC AER29796;
 XX
 DT 11-JUN-2007 (revised)
 DT 22-MAR-2007 (first entry)
 XX
 DE Breast cancer-associated gene SEQ ID NO:97.
 XX
 KW diagnosis; breast tumor; biochip; tumor marker; genetic marker;
 KW biomarker; DNA detection; RNA detection; ds; PIK3CA.
 XX
 OS Homo sapiens.
 XX
 PN WO2007006911-A2.
 XX
 PD 18-JAN-2007.
 XX
 PF 05-JUL-2006; 2006WO-FR001593.
 XX
 PR 07-JUL-2005; 2005FR-00052087.
 XX
 PA (INMR) BIOMERIEUX SA.
 XX
 PI Krause A, Leissner P, Mougin B, Paye M;
 XX
 DR WPI; 2007-138577/14.
 DR PC:NCBI; gi54792081.
 DR PC_ENCPRO:NCBI; gi54792082.
 XX
 PT In vitro diagnosis of breast cancer comprises extracting biological
 PT material of biological sample, contacting biological material with
 PT specific reagents of target genes and determining target gene expression.
 XX
 PS Example 2; SEQ ID NO 97; 305pp; French.
 XX
 CC The invention describes a method for in vitro diagnosis of breast cancer
 CC in a patient susceptible to be affected by breast cancer, comprising:
 CC extracting nucleic acid from a biological sample taken from the patient;
 CC contacting the nucleic acid with at least 8 hybridization probes for
 CC detection of target genes chosen from SEQ ID Nos. 1 to 8 or 10 probes for
 CC detection of target genes chosen from SEQ ID Nos. 1, 2, 4, 6, 13, 14, 26,
 CC 69, 81 and 105; and determining the expression of the target genes. The
 CC invention also includes: a support, such as a biochip, comprising at
 CC least 8 or 10 hybridization probes mentioned above; and a diagnosis kit
 CC for breast cancer comprising the support. The method, biochip and kit are
 CC useful for the in vitro diagnosis of breast cancer. This sequence is a
 CC breast cancer-associated gene.
 CC
 CC Revised record issued on 11-JUN-2007 : Enhanced with precomputed
 CC information from BOND.

XX

SQ Sequence 3724 BP; 1242 A; 684 C; 763 G; 1035 T; 0 U; 0 Other;

Query Match 97.5%; Score 3339.6; DB 5; Length 3724;
 Best Local Similarity 98.8%;
 Matches 3385; Conservative 0; Mismatches 39; Indels 2; Gaps 2;

Qy	1	AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAAGTGTGGGGCATCCACTTGATG	60
Db	146	AGAATCAGAACAATGCCTCCACGACCATCATCAGGTGAAGTGTGGGGCATCCACTTGATG	205
Qy	61	CCCCAAGAATCCTAGTGAATGTTTACTACCAATGGAATGATAGTGACTTTAGAATGC	120
Db	206	CCCCAAGAATCCTAGTAGAATGTTTACTACCAATGGAATGATAGTGACTTTAGAATGC	265
Qy	121	CTCCGTGAGGCTACATTAGTAACATAAAGCATGAACATTTTAAAGAAGCAAGAAAATAC	180
Db	266	CTCCGTGAGGCTACATTAATAACCATAAAGCATGAACATTTTAAAGAAGCAAGAAAATAC	325
Qy	181	CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAGAA	240
Db	326	CCCCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACTCAAGAA	385
Qy	241	GCAGAAAGGGAAGAATTTTTTGTATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAA	300
Db	386	GCAGAAAGGGAAGAATTTTTTGTATGAAACAAGACGACTTTGTGACCTTCGGCTTTTTCAA	445
Qy	301	CCATTTTTTAAAGTAATTGAACCAAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Db	446	CCCTTTTTTAAAGTAATTGAACCAAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	505
Qy	361	ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTGATATGGTTAAAGATCCTGAAGTA	420
Db	506	ATTGGTTTTGCTATCGGCATGCCAGTGTGGAATTGATATGGTTAAAGATCCAGAAGTA	565
Qy	421	CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAGAAGCTGTGGATCTTAGGGATCTT	480
Db	566	CAGGACTTCCGAAGAAATATTCTGAACGTTTGTAAGAAGCTGTGGATCTTAGGGACCTC	625
Qy	481	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG	540
Db	626	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCTCCAAATGTAGAATCTTCACCAGAA	685
Qy	541	CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTA	600
Db	686	TTGCCAAAGCACATATATAATAAATTAGATAAAGGGCAAATAATAGTGGTGATCTGGGTA	745
Qy	601	ATAGTTTCTCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG	660

Db	746	ATAGTTCCTCCAAATAATGACAAGCAGAAGTATACTCTGAAATCAACCATGACTGTGTA	805
Qy	661	CCAGAACAAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAAGTATGTTGCTATCATCT	720
Db	806	CCAGAACAAAGTAATTGCTGAAGCAATCAGGAAAAAACTCGAAGTATGTTGCTATCCTCT	865
Qy	721	GAACAATTAATACTCTGTGTTTTAGAAATATCAGGGCAAGTACATTTTAAAGTGTGTGGA	780
Db	866	GAACAATTAATACTCTGTGTTTTAGAAATATCAGGGCAAGTATATTTTAAAGTGTGTGGA	925
Qy	781	TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Db	926	TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	985
Qy	841	ATAATGCTTGGGAGGATGCCCAATTGGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Db	986	ATAATGCTTGGGAGGATGCCCAATTGATGTTGATGGCTAAAGAAAGCCTTTATTCTCAA	1045
Qy	901	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCAGACGCATTTCACAGCTACACCA	960
Db	1046	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCAGACGCATTTCACAGCTACACCA	1105
Qy	961	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA	1020
Db	1106	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGTGCCTCAGAATA	1165
Qy	1021	AAAATTCCTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT	1080
Db	1166	AAAATTCCTTGTGCAACCTACGTGAATGTAAATATTCGAGACATTGATAAGATCTATGTT	1225
Qy	1081	CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Db	1226	CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA	1285
Qy	1141	CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCTGATCTT	1200
Db	1286	CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCTGATCTT	1345
Qy	1201	CCTCGTGTGCTCGACTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA	1260
Db	1346	CCTCGTGTGCTCGACTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA	1405
Qy	1261	GAGGAACACTGTCCATTGGCATGGGGAAATATAAAGTGTGTTGATTACAGACACTCTA	1320
Db	1406	GAGGAACACTGTCCATTGGCATGGGGAAATATAAAGTGTGTTGATTACAGACACTCTA	1465
Qy	1321	GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTGCTG	1380
Db	1466	GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTGCTG	1525

Qy	1381	AACCCATTGGTGTACTGGATCAAATCAAATAAAGAAACTCCATGCTTAGAGTTGGAG	1440
Db	1526	AACCCATTGGTGTACTGGATCAAATCAAATAAAGAAACTCCATGCTTAGAGTTGGAG	1585
Qy	1441	TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Db	1586	TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCAGATATGTCAGTGATTGAAGAGCATGCC	1645
Qy	1501	AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Db	1646	AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1705
Qy	1561	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620
Db	1706	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1765
Qy	1621	CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAAGATTTTCTATGGAGTCACAGACAC	1680
Db	1766	CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAAGATTTTCTATGGAGTCACAGACAC	1825
Qy	1681	TATTGTGTAACACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT	1740
Db	1826	TATTGTGTAACACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT	1885
Qy	1741	AGAGATGAAGTAGCCAGATGTATTGCTTGGTAAAAGATTGGCTCCAATCAAACCTGAA	1800
Db	1886	AGAGATGAAGTAGCCAGATGTATTGCTTGGTAAAAGATTGGCTCCAATCAAACCTGAA	1945
Qy	1801	CAGGCTATGGAACCTCTGAGCTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT	1860
Db	1946	CAGGCTATGGAACCTCTGAGCTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT	2005
Qy	1861	CGGTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA	1920
Db	2006	CGGTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA	2065
Qy	1921	CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTACTGAAGAAA	1980
Db	2066	CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTACTGAAGAAA	2125
Qy	1981	GCATTGACTAATCAAAGGATTGGGCACCTTTTCTTTTGGCATTTAAATCTGAGATGCAC	2040
Db	2126	GCATTGACTAATCAAAGGATTGGGCACCTTTTCTTTTGGCATTTAAATCTGAGATGCAC	2185
Qy	2041	AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2100
Db	2186	AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2245

Qy	2101	ATGTATTTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACTTAACT	2160
Db	2246	ATGTATTTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACTTAACT	2305
Qy	2161	GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTAGTT	2220
Db	2306	GACATTCTCAAACAGGAGAGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTAGTT	2365
Qy	2221	GAGCAAAATGAGGCGACCAGATTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC	2280
Db	2366	GAGCAAAATGAGGCGACCAGATTTCATGGATGCTCTACAGGGCTTCTGTCTCCTCTAAAC	2425
Qy	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTGCAATTATGTCTTCTGCAAAA	2340
Db	2426	CCTGCTCATCAACTAGGAAACCTCAGGCTTGAAGAGTGTGCAATTATGTCTTCTGCAAAA	2485
Qy	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTGAGATTACTGTTTCAGAAC	2400
Db	2486	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTGAGATTACTGTTTCAGAAC	2545
Qy	2401	AATGAGATCATCTTTAAAAATGGGGATGATTACGGCAAGATATGCTAACACTTCAAATT	2460
Db	2546	AATGAGATCATCTTTAAAAATGGGGATGATTACGGCAAGATATGCTAACACTTCAAATT	2605
Qy	2461	ATTTCGTATTATGAAAAATATCTGGCAAAATCAAGGCTTGATCTTCGAATGTTACCTTAT	2520
Db	2606	ATTTCGTATTATGAAAAATATCTGGCAAAATCAAGGCTTGATCTTCGAATGTTACCTTAT	2665
Qy	2521	GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCACACT	2580
Db	2666	GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCACACT	2725
Qy	2581	ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2640
Db	2726	ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2785
Qy	2641	CTACATCAGTGGCTCAAAGACAAGAACAAGGAGAAATATATGATGCAGCCATTGACCTG	2700
Db	2786	CTACATCAGTGGCTCAAAGACAAGAACAAGGAGAAATATATGATGCAGCCATTGACCTG	2845
Qy	2701	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760
Db	2846	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2905
Qy	2761	CACAATAGTAACATCATGGTGAAAGACGATGGACAACCTGTTTCATATAGATTTGGACAC	2820
Db	2906	CACAATAGTAACATCATGGTGAAAGACGATGGACAACCTGTTTCATATAGATTTGGACAC	2965
Qy	2821	TTTTTGGATCACAGAAGAAAAAATTGGTTTATAAACGAGAAGCTGTGCCATTTGTTTTG	2880

Db	2966	TTTTTGGATCACAAGAAGAAAAAATTGGTTATAAACGAGAACGTGTGCCATTGTGTTTG	3025
Qy	2881	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940
Db	3026	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	3085
Qy	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT	3000
Db	3086	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT	3145
Qy	3001	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060
Db	3146	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3205
Qy	3061	GATGACATTGCATACATTGAAAGACCCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG	3120
Db	3206	GATGACATTGCATACATTGAAAGACCCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG	3265
Qy	3121	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Db	3266	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3325
Qy	3181	TGGATCTTCCACACAATTAACAGCATGCATTGAACTG-AAAGATAACTGAGAAAAATGAA	3239
Db	3326	TGGATCTTCCACACAATTAACAGCATGCATTGAACTGAAAAGATAACTGAGAAAAATGAA	3385
Qy	3240	AGCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGC	3299
Db	3386	AGCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGC	3445
Qy	3300	ATAGGAATTGCACAATCCATGAACAGCATTAG-ATTACAGCAAGAACAGAAATAAAATA	3358
Db	3446	ATAGGAATTGCACAATCCATGAACAGCATTAGAAATTACAGCAAGAACAGAAATAAAATA	3505
Qy	3359	CTATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAACTAGTTCATT	3418
Db	3506	CTATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAACTAGTTCATT	3565
Qy	3419	TCAAAA 3424	
Db	3566	TCAAAA 3571	

RESULT 14

ARV60468

ID ARV60468 standard; cDNA; 3724 BP.

XX

AC ARV60468;

XX
DT 24-JUL-2008 (first entry)
XX
DE Human PIK3CA polynucleotide, SEQ ID 30.
XX
KW mutation; dna microarray; prognosis; diagnostic test; therapeutic;
KW non-small-cell lung cancer; tumor; cytostatic; ss; gene;
KW phosphoinositide-3-kinase, catalytic, alpha polypeptide; PIK3CA.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 158..3364
FT /*tag= a
FT /product
XX
PN WO2008061213-A2.
XX
PD 22-MAY-2008.
XX
PF 15-NOV-2007; 2007WO-US084888.
XX
PR 16-NOV-2006; 2006US-0866103P.
PR 10-JUL-2007; 2007US-0948818P.
XX
PA (GETH) GENENTECH INC.
XX
PI Seshagiri S, Peters B, Kan Z;
XX
DR WPI; 2008-G25985/39.
DR P-PSDB; ARV60505.
DR PC:NCBI; gi54792081.
DR PC_ENCPRO:NCBI; gi54792082.
XX
PT New isolated polynucleotide comprises PRO polynucleotide or fragment
PT comprising a nucleotide variation, useful for detecting nucleotide
PT variations for diagnosing and treating tumors.
XX
PS Claim 2; SEQ ID NO 30; 55pp; English.
XX
CC The present invention relates to a novel isolated polynucleotide
CC comprising a PRO polynucleotide or its fragment. The PRO polynucleotide
CC or its fragment comprises a nucleotide variation at a nucleotide position
CC given in the specification. A nucleotide variation refers to a change in
CC a nucleotide sequence (e.g., an insertion, deletion, inversion, or
CC substitution of one or more nucleotides, such as a single nucleotide
CC polymorphism (SNP)) relative to a reference sequence (e.g., a wild type
CC sequence). A nucleotide variation may be a somatic mutation or a germline
CC polymorphism. The present invention provides: (i) an allele-specific

CC oligonucleotide that hybridizes to a region of a PRO polynucleotide
 CC comprising a nucleotide variation at a nucleotide position, or its
 CC complement; (iii) a kit comprising the oligonucleotide and an enzyme;
 CC (iii) a microarray comprising the oligonucleotide; (iv) a method for
 CC detecting the absence or presence of the variation at a nucleotide
 CC position; (v) a method for amplifying a nucleic acid comprising the
 CC nucleotide variation; (vi) a method for determining the genotype of a
 CC biological sample (e.g. non-small cell lung carcinoma sample) from a
 CC mammal; (vii) a method for classifying a tumor in the mammal; and (viii)
 CC a method for predicting whether a tumor (e.g. non-small cell lung
 CC carcinoma) will respond to a therapeutic agent that targets a PRO or a
 CC PRO polynucleotide, comprises determining whether the tumor comprises a
 CC variation in a PRO or PRO polynucleotide, where the presence of a
 CC variation indicates that the tumor will respond to the therapeutic agent.
 CC The method of detecting the absence or presence of the nucleotide
 CC variation comprises: (a) contacting the suspected nucleic acid with the
 CC allele-specific oligonucleotide that is specific for the nucleotide
 CC variation, under conditions suitable for hybridization of the
 CC oligonucleotide to the nucleic acid; and (b) detecting the absence or
 CC presence of allele-specific hybridization. The method of amplifying the
 CC nucleic acid comprising the nucleotide variation comprises: (a)
 CC contacting the nucleic acid with a primer that hybridizes to the nucleic
 CC acid at 3' of the nucleotide variation; and (b) extending the primer to
 CC generate an amplification product comprising the nucleotide variation.
 CC The isolated polynucleotide is used for detecting nucleotide variations.
 CC The methods are used for diagnosing and treating tumors. The present
 CC sequence is a human PRO polynucleotide sequence used in the invention.
 CC
 CC Revised record issued on 18-JUN-2008 : Enhanced with precomputed
 CC information from BOND.

XX

SQ Sequence 3724 BP; 1242 A; 684 C; 763 G; 1035 T; 0 U; 0 Other;

Query Match 97.5%; Score 3339.6; DB 7; Length 3724;
 Best Local Similarity 98.8%;
 Matches 3385; Conservative 0; Mismatches 39; Indels 2; Gaps 2;

Qy 1 AGGATCAGAACAAATGCCTCCAAGACCATCATCAGGTGAAGTGTGGGGCATCCACTTGATG 60
 || |||||
 Db 146 AGAATCAGAACAAATGCCTCCACGACCATCATCAGGTGAAGTGTGGGGCATCCACTTGATG 205
 Qy 61 CCCCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC 120
 |||||
 Db 206 CCCCCAAGAATCCTAGTAGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC 265
 Qy 121 CTCCTGAGGCTACATTAGTAAGTATAAAGCATGAAGTATTTAAAGAAGCAAGAAAATAC 180
 |||||
 Db 266 CTCCTGAGGCTACATTAAATAACCATAAAGCATGAAGTATTTAAAGAAGCAAGAAAATAC 325

Qy	181	CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTACCCAGAA	240
Db	326		385
Qy	241	GCAGAAAGGGAAGAATTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTCAA	300
Db	386		445
Qy	301	CCATTTTTAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Db	446		505
Qy	361	ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTGATATGGTTAAAGATCCTGAAGTA	420
Db	506		565
Qy	421	CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAGAAGCTGTGGATCTTAGGGATCTT	480
Db	566		625
Qy	481	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG	540
Db	626		685
Qy	541	CTGCCAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTA	600
Db	686		745
Qy	601	ATAGTTTCTCCAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG	660
Db	746		805
Qy	661	CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAAGTATGTTGCTATCATCT	720
Db	806		865
Qy	721	GAACAATTAAGTCTGTGTTTTAGAAATATCAGGGCAAGTACATTTTAAAGTGTGTGGA	780
Db	866		925
Qy	781	TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Db	926		985
Qy	841	ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Db	986		1045
Qy	901	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	960

Db	1046		CTGCCAATGGACTGTTTTACAATGCCATCTTATTCAGACGCATTTCACAGCTACACCA	1105
Qy	961		TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA	1020
Db	1106		TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGTGCACCTCAGAATA	1165
Qy	1021		AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT	1080
Db	1166		AAAATTCTTTGTGCAACCTACGTGAATGTAAATATTCGAGACATTGATAAGATCTATGTT	1225
Qy	1081		CGAACAGGTATCTACCATGGAGGAGAACCCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Db	1226		CGAACAGGTATCTACCATGGAGGAGAACCCCTTATGTGACAATGTGAACACTCAAAGAGTA	1285
Qy	1141		CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCTGATCTT	1200
Db	1286		CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCTGATCTT	1345
Qy	1201		CCTCGTGTGCTCGACTTTGCCTTTCCATTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA	1260
Db	1346		CCTCGTGTGCTCGACTTTGCCTTTCCATTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA	1405
Qy	1261		GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACAGACACTCTA	1320
Db	1406		GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACAGACACTCTA	1465
Qy	1321		GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTGCTG	1380
Db	1466		GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTGCTG	1525
Qy	1381		AACCTTATTGGTGTTACTGGATCAAATCCAAATAAGAAACTCCATGCTTAGAGTTGGAG	1440
Db	1526		AACCTTATTGGTGTTACTGGATCAAATCCAAATAAGAAACTCCATGCTTAGAGTTGGAG	1585
Qy	1441		TTTGAAGTGGTTTCTGAGTGTGGTAAAGTTCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Db	1586		TTTGAAGTGGTTTCTGAGTGTGGTAAAGTTCCAGATATGTCAGTGATTGAAGAGCATGCC	1645
Qy	1501		AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Db	1646		AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1705
Qy	1561		CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620
Db	1706		CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1765
Qy	1621		CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAAGATTTTCTATGGAGTCACAGACAC	1680

Db	1766	CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC	1825
Qy	1681	TATTGTGTAACATATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT	1740
Db	1826	TATTGTGTAACATATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT	1885
Qy	1741	AGAGATGAAGTAGCCAGATGTATTGCTTGGTAAAGATTGGCCTCCAATCAAACCTGAA	1800
Db	1886	AGAGATGAAGTAGCCAGATGTATTGCTTGGTAAAGATTGGCCTCCAATCAAACCTGAA	1945
Qy	1801	CAGGCTATGGAACCTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTGTCTGTT	1860
Db	1946	CAGGCTATGGAACCTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTGTCTGTT	2005
Qy	1861	CGGTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA	1920
Db	2006	CGGTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA	2065
Qy	1921	CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTACTGAAGAAA	1980
Db	2066	CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTACTGAAGAAA	2125
Qy	1981	GCATTGACTAATCAAAGGATTGGGCACCTTTTCTTTTGGCATTAAAACTGAGATGCAC	2040
Db	2126	GCATTGACTAATCAAAGGATTGGGCACCTTTTCTTTTGGCATTAAAACTGAGATGCAC	2185
Qy	2041	AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2100
Db	2186	AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2245
Qy	2101	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTAACT	2160
Db	2246	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTAACT	2305
Qy	2161	GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTAGTT	2220
Db	2306	GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTAGTT	2365
Qy	2221	GAGCAAATGAGGCGACCAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC	2280
Db	2366	GAGCAAATGAGGCGACCAGATTTTCATGGATGCTCTACAGGGCTTTCTGTCTCCTCTAAAC	2425
Qy	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTGCAATTATGTCTTCTGCAAAA	2340
Db	2426	CCTGCTCATCAACTAGGAAACCTCAGGCTTGAAGAGTGTGCAATTATGTCTTCTGCAAAA	2485
Qy	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTGCAGAGTTACTGTTTCAGAAC	2400
Db	2486	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTGCAGAGTTACTGTTTCAGAAC	2545

Qy	2401	AATGAGATCATCTTTAAAAATGGGGATGATTACGGCAAGATATGCTAACACTTCAAATT	2460
Db	2546	AATGAGATCATCTTTAAAAATGGGGATGATTACGGCAAGATATGCTAACACTTCAAATT	2605
Qy	2461	ATTCGTATTATGAAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT	2520
Db	2606	ATTCGTATTATGAAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT	2665
Qy	2521	GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTTCTCAGCT	2580
Db	2666	GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTTCTCAGCT	2725
Qy	2581	ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2640
Db	2726	ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2785
Qy	2641	CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG	2700
Db	2786	CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG	2845
Qy	2701	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760
Db	2846	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2905
Qy	2761	CACAATAGTAACATCATGGTGAAAGACGATGGACAACCTGTTTCATATAGATTTTGGACAC	2820
Db	2906	CACAATAGTAACATCATGGTGAAAGACGATGGACAACCTGTTTCATATAGATTTTGGACAC	2965
Qy	2821	TTTTTGGATCACAAGAAGAAAAAATTGTTTATATAACGAGACGTGTGCCATTTGTTTTG	2880
Db	2966	TTTTTGGATCACAAGAAGAAAAAATTGTTTATATAACGAGACGTGTGCCATTTGTTTTG	3025
Qy	2881	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940
Db	3026	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	3085
Qy	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT	3000
Db	3086	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT	3145
Qy	3001	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060
Db	3146	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3205
Qy	3061	GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAACTGAGCAAGAGGCTTTG	3120
Db	3206	GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAACTGAGCAAGAGGCTTTG	3265

Qy	3121	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAAACAAAATGGAT	3180
Db	3266	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAAACAAAATGGAT	3325
Qy	3181	TGGATCTTCCACACAATTAACAGCATGCATTGAACTG-AAAGATAACTGAGAAAATGAA	3239
Db	3326	TGGATCTTCCACACAATTAACAGCATGCATTGAACTGAAAAGATAACTGAGAAAATGAA	3385
Qy	3240	AGCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGC	3299
Db	3386	AGCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGC	3445
Qy	3300	ATAGGAATTGCACAATCCATGAACAGCATTAG-ATTACAGCAAGAACAGAAATAAAATA	3358
Db	3446	ATAGGAATTGCACAATCCATGAACAGCATTAGAATTTACAGCAAGAACAGAAATAAAATA	3505
Qy	3359	CTATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAACTAGTTCATT	3418
Db	3506	CTATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAACTAGTTCATT	3565
Qy	3419	TCAAAA 3424	
Db	3566	TCAAAA 3571	

RESULT 15

ARW65283

ID ARW65283 standard; cDNA; 3724 BP.

XX

AC ARW65283;

XX

DT 07-AUG-2008 (first entry)

XX

DE Human PIK3CA cDNA, SEQ ID 53.

XX

KW tumor marker; prognosis; diagnostic test; cancer; ss; gene; PIK3CA.

XX

OS Homo sapiens.

XX

PN WO2008070325-A2.

XX

PD 12-JUN-2008.

XX

PF 24-OCT-2007; 2007WO-US082397.

XX

PR 26-OCT-2006; 2006US-0863106P.

PR

PR 14-MAY-2007; 2007US-0917814P.

XX

PA (GETH) GENENTECH INC.

XX

PI Kan Z, Kenski DM, Peters B, Seshagiri S;

XX

DR WPI; 2008-G69314/42.

DR P-PSDB; ARW65361.

DR PC:NCBI; gi54792081.

DR PC_ENCPRO:NCBI; gi54792082.

XX

PT New polynucleotide, useful for determining the genotype of a sample from
PT a mammal, for classifying a tumor in a mammal or for predicting whether a
PT tumor will respond to a therapeutic agent that targets a PRO polypeptide
PT or polynucleotide.

XX

PS Claim 2; SEQ ID NO 53; 98pp; English.

XX

CC The present invention relates to novel isolated polynucleotides. An
CC isolated polynucleotide comprises: (a) a PRO polynucleotide or its
CC fragment that is at least about 10 nucleotides in length or that
CC comprises a nucleotide variation at a nucleotide position given in the
CC specification, or (b) its complement. These variations provide biomarkers
CC for cancer and/or predisposition to tumorigenesis or tumor promotion. The
CC present invention provides: (1) a kit comprising the oligonucleotide and
CC at least one enzyme; (2) a microarray comprising the oligonucleotide; (3)
CC a method for detecting the absence or presence of a nucleotide variation
CC at a nucleotide position given in the specification, which comprises
CC contacting the nucleic acid suspected of comprising the nucleotide
CC variation with an allele-specific oligonucleotide that is specific for
CC the nucleotide variation and detecting the absence or presence of allele-
CC specific hybridization; (4) a method for amplifying a nucleic acid
CC comprising a nucleotide variation at a nucleotide position given in the
CC specification; (5) a method for determining the genotype of a tumor
CC sample from a mammal; (6) a method for classifying a tumor in a mammal by
CC detecting the presence of a variation in a PRO or PRO polynucleotide in a
CC biological sample derived from the mammal; and (7) a method for
CC predicting whether a tumor will respond to a therapeutic agent that
CC targets a PRO or a PRO polynucleotide by determining whether the tumor
CC comprises a variation in a PRO or PRO polynucleotide, where the presence
CC of a variation indicates that the tumor will respond to the therapeutic
CC agent. The method of amplifying a nucleic acid comprising a nucleotide
CC variation comprises: (a) contacting the nucleic acid with a primer that
CC hybridizes to the nucleic acid at a sequence 3' of the nucleotide
CC variation, and (b) extending the primer to generate an amplification
CC product comprising the nucleotide variation. The variations disclosed in
CC the invention are useful in methods and compositions related to cancer
CC diagnosis and therapy. The present sequence is an isolated polynucleotide
CC of the invention.

CC

CC Revised record issued on 09-JUL-2008 : Enhanced with precomputed infor

CC

cc

CC Revised record issued on 09-JUL-2008 : mation from BOND.

XX

SQ Sequence 3724 BP; 1242 A; 684 C; 763 G; 1035 T; 0 U; 0 Other;

Query Match	97.5%;	Score	3339.6;	DB	7;	Length	3724;
Best Local Similarity	98.8%;						
Matches	3385;	Conservative	0;	Mismatches	39;	Indels	2;
				Gaps	2;		

Qy 1 AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAAC TGTGGGGCATCCACTTGATG 60
 | | | | | | | | | | | | | | | | | | | | | |
Db 146 AGAATCAGAACAATGCCTCCAGACCATCATCAGGTGAAC TGTGGGGCATCCACTTGATG 205

Qy 61 CCCCCAAGAATCCTAGTGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC 120
|||||
Db 206 CCCCCAAGAATCCTAGTAGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC 265

Qy 121 CTCCGTGAGGCTACATTAGTAACATATAAAGCATGAAC TATTTAAAGAAGCAAGAAAATAC 180
|||||
Db 266 CTCCGTGAGGCTACATTAATAACCATAAAGCATGAAC TATTTAAAGAAGCAAGAAAATAC 325

Qy 181 CCTCTCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA 240
|| ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||

Db 326 CCCCTCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACTCAAGAA 385

Qy 241 GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTCAA 300
|||||
Db 386 GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGACCTTCGGCTTTTCAA 445

Qy 301 CCATTTTAAAAAGTAATTGAACCAAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA 360
|||
Db 446 CCCTTTTAAAAAGTAATTGAACCAAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA 505

Qy 361 ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTGATATGGTTAAAGATCCTGAAGTA 420
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 506 ATTGGTTTTGCTATCGGCATGCCAGTGTGTGAATTGATATGGTTAAAGATCCAGAAGTA 565

Qy 421 CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAAGAGCTGTGGATCTTAGGGATCTT 480
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 566 CAGGACTTCCGAAGAAATATTCTGAACGTTGTAAAGAGCTGTGGATCTTAGGGACCTT 625

Qy 481 AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG 540
 |||
 Db 626 AATTCACCTCATAGTAGAGCAATGTATGTCTATCCTCCAAATGTAGAATCTTCACCAGAA 685

Qy 541 CTGCCAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTGGGTA 600
|||||
Db 686 TTGCCAAGCACATATATAATAAATTAGATAAAGGGCAAATAATAGTGGTGATCTGGGTA 745

Qy	601	ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAATCAACCATGACTGTGTG	660
Db	746	ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAATCAACCATGACTGTGTA	805
Qy	661	CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT	720
Db	806	CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTCGAAGTATGTTGCTATCCTCT	865
Qy	721	GAACAATTAATACTCTGTGTTTTAGAAATATCAGGCAAGTACATTTTAAAGTGTGTGGA	780
Db	866	GAACAATAATACTCTGTGTTTTAGAAATATCAGGCAAGTATATTTTAAAGTGTGTGGA	925
Qy	781	TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Db	926	TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	985
Qy	841	ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Db	986	ATAATGCTTGGGAGGATGCCCAATTTGATGTTGATGGCTAAAGAAAGCCTTTATTCTCAA	1045
Qy	901	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCAGACGCATTTCCACAGCTACACCA	960
Db	1046	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCAGACGCATTTCCACAGCTACACCA	1105
Qy	961	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA	1020
Db	1106	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGTGCCTCAGAATA	1165
Qy	1021	AAAATCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT	1080
Db	1166	AAAATCTTTGTGCAACCTACGTGAATGTAAATATTCGAGACATTGATAAGATCTATGTT	1225
Qy	1081	CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Db	1226	CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA	1285
Qy	1141	CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCTGATCTT	1200
Db	1286	CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCTGATCTT	1345
Qy	1201	CCTCGTGTGCTCGACTTTGCCTTTCCATTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA	1260
Db	1346	CCTCGTGTGCTCGACTTTGCCTTTCCATTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA	1405
Qy	1261	GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACAGACACTCTA	1320
Db	1406	GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACAGACACTCTA	1465
Qy	1321	GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1380

Db	1466		GTATCTGGAAAAATGGCTTTGAACTTTGGCCAGTACCTCATGGATTAGAAGATTGCTG	1525
Qy	1381		AACCCTATTGGTGTACTGGATCAAATCCAAATAAGAACTCCATGCTTAGAGTTGGAG	1440
Db	1526		AACCCTATTGGTGTACTGGATCAAATCCAAATAAGAACTCCATGCTTAGAGTTGGAG	1585
Qy	1441		TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCGAGATATGTCAGTGATTGAAGAGCATGCC	1500
Db	1586		TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCGAGATATGTCAGTGATTGAAGAGCATGCC	1645
Qy	1501		AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCACGCAGGACTGAGTAACAGA	1560
Db	1646		AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCACGCAGGACTGAGTAACAGA	1705
Qy	1561		CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620
Db	1706		CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1765
Qy	1621		CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAAGATTTTCTATGGAGTCACAGACAC	1680
Db	1766		CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAAGATTTTCTATGGAGTCACAGACAC	1825
Qy	1681		TATTGTGTAACATATCCCCGAAATTTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTTCT	1740
Db	1826		TATTGTGTAACATATCCCCGAAATTTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTTCT	1885
Qy	1741		AGAGATGAAGTAGCCAGATGTATTGCTTGGTAAAAGATTGGCTCCAATCAAACCTGAA	1800
Db	1886		AGAGATGAAGTAGCCAGATGTATTGCTTGGTAAAAGATTGGCTCCAATCAAACCTGAA	1945
Qy	1801		CAGGCTATGGAATCTCTGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT	1860
Db	1946		CAGGCTATGGAATCTCTGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT	2005
Qy	1861		CGGTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA	1920
Db	2006		CGGTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA	2065
Qy	1921		CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA	1980
Db	2066		CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA	2125
Qy	1981		GCATTGACTAATCAAAGGATTGGGCACCTTTTCTTTTGGCATTTAAATCTGAGATGCAC	2040
Db	2126		GCATTGACTAATCAAAGGATTGGGCACCTTTTCTTTTGGCATTTAAATCTGAGATGCAC	2185
Qy	2041		AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2100

Db	2186	AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTCGATGTGGG	2245
Qy	2101	ATGTATTTGAAGCACCTGAATAGGCCAAGTCGAGGCAATGGAAAAGCTCATTAACTTAACT	2160
Db	2246	ATGTATTTGAAGCACCTGAATAGGCCAAGTCGAGGCAATGGAAAAGCTCATTAACTTAACT	2305
Qy	2161	GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTAGTT	2220
Db	2306	GACATTCTCAAACAGGAGGAAGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTAGTT	2365
Qy	2221	GAGCAATGAGGCGACCAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC	2280
Db	2366	GAGCAATGAGGCGACCAGATTTTCATGGATGCTCTACAGGGCTTTCTGTCTCCTCTAAAC	2425
Qy	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTGCAATTATGTCTTCTGCAAAA	2340
Db	2426	CCTGCTCATCAACTAGGAAACCTCAGGCTTGAAGAGTGTGCAATTATGTCTTCTGCAAAA	2485
Qy	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTGAGGTTACTGTTTCAGAAC	2400
Db	2486	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTGAGGTTACTGTTTCAGAAC	2545
Qy	2401	AATGAGATCATCTTTAAAAATGGGGATGATTACGGCAAGATATGCTAACACTTCAAATT	2460
Db	2546	AATGAGATCATCTTTAAAAATGGGGATGATTACGGCAAGATATGCTAACACTTCAAATT	2605
Qy	2461	ATTCGTATTATGAAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT	2520
Db	2606	ATTCGTATTATGAAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT	2665
Qy	2521	GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT	2580
Db	2666	GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT	2725
Qy	2581	ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2640
Db	2726	ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2785
Qy	2641	CTACATCAGTGGCTCAAAGACAAGAACAAGGAGAAATATATGATGCAGCCATTGACCTG	2700
Db	2786	CTACATCAGTGGCTCAAAGACAAGAACAAGGAGAAATATATGATGCAGCCATTGACCTG	2845
Qy	2701	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760
Db	2846	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2905
Qy	2761	CACAATAGTAACATCATGGTGAAAGACGATGGACAACCTGTTTCATATAGATTTGGACAC	2820
Db	2906	CACAATAGTAACATCATGGTGAAAGACGATGGACAACCTGTTTCATATAGATTTGGACAC	2965

Qy	2821	TTTTTGGATCACAGAAGAAAAAATTGGTTATAAACGAGAACGTGTGCCATTGTGTTTTG	2880
Db	2966	TTTTTGGATCACAGAAGAAAAAATTGGTTATAAACGAGAACGTGTGCCATTGTGTTTTG	3025
Qy	2881	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940
Db	3026	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	3085
Qy	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT	3000
Db	3086	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT	3145
Qy	3001	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060
Db	3146	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3205
Qy	3061	GATGACATTGCATACATTGCGAAAGCCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG	3120
Db	3206	GATGACATTGCATACATTGCGAAAGCCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG	3265
Qy	3121	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Db	3266	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3325
Qy	3181	TGGATCTTCCACACAATTAAACAGCATGCATTGAACTG-AAAGATAACTGAGAAAAATGAA	3239
Db	3326	TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAAGATAACTGAGAAAAATGAA	3385
Qy	3240	AGCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAGACCGATTGC	3299
Db	3386	AGCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAGACCGATTGC	3445
Qy	3300	ATAGGAATTGCACAATCCATGAACAGCATTAG-ATTACAGCAAGAACAGAAATAAAATA	3358
Db	3446	ATAGGAATTGCACAATCCATGAACAGCATTAGAATTACAGCAAGAACAGAAATAAAATA	3505
Qy	3359	CTATATAATTTAAATAATGTAAACGCAACAGGGTTTGATAGCACTTAACTAGTTCATT	3418
Db	3506	CTATATAATTTAAATAATGTAAACGCAACAGGGTTTGATAGCACTTAACTAGTTCATT	3565
Qy	3419	TCAAAA 3424	
Db	3566	TCAAAA 3571	

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